

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 05-01-03
Searcher: Beverly E 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ _____ Other CGN

GenCore version 5.1.4 p5 4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2003, 09:41:39 ; Search time 3394 Seconds

(without alignments)
5890.874 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVSVLYFYGILOSDA.....SALALHFTLSNNNDPYIL 687

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPTO/spool/US10061727/runat_23042003_083116_7892/app_query.fasta_1.839
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: GenEmbl:*

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- 2: gb_hcg:*
- 3: gb_in:*
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29: em_vi:*

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31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rtd:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hgo_hum:*

40: em_hgo_mus:*

41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2591.5	70.6	4724	9 AB006537	AB006537 Homo sapi
2	2586	70.5	1740	6 AR166115	AR166115 Sequence
3	2586	70.5	1740	9 AF029213	AF029213 Homo sapi
4	2327.5	63.4	3355	6 AR166116	AR166116 Sequence
5	2327.5	63.4	3355	10 NM111RACP	X85999 M. musculus
6	2313.5	63.1	1862	10 RNU48592	U48592 Rattus norv
7	1892	51.6	1857	9 AF167343	AF167343 Homo sapi
8	1663	45.3	1916	10 BC021159	BC021159 Mus muscu
9	1368	37.3	2226	9 AK095107	AK095107 Homo sapi
10	1256	34.2	46509	9 AC108747	AC108747 Homo sapi
11	1042	28.4	58987	2 AC119283	AC119283 Mus muscu
12	825	22.5	2061	6 AR179668	AR179668 Sequence
13	825	22.5	2061	9 AF212016	AF212016 Homo sapi
14	825	22.5	2080	9 HSA290436	AJ290436 Homo sapi
15	825	22.5	2212	9 AF284436	AF284436 Homo sapi
16	825	22.5	2985	9 HSA272208	AJ272208 Homo sapi
17	817.5	22.0	1979	9 AF181285	AF181285 Homo sapi
18	806.5	22.0	2518	10 AF284437	AF284437 Mus muscu
19	800	21.8	1737	6 AR179667	AR179667 Sequence
20	774	21.1	2722	9 AF181284	AF181284 Homo sapi
21	772	21.0	2258	9 AF284435	AF284435 Homo sapi
22	772	21.0	3504	9 HSA243874	AJ243874 Homo sapi
23	767	20.9	2537	6 AR179677	AR179677 Sequence
24	536	14.6	890	9 F167335S04	AF167336 Homo sapi
25	536	14.6	184203	9 AC008249	AC008249 Homo sapi
26	531	14.5	87015	2 AC098400	AC098400 Rattus no
27	528.5	14.4	1620	6 AR102826	AR102826 Sequence
28	528.5	14.4	1620	6 E26338	E26338 Polypeptide
29	528	14.4	1626	6 AR016447	AR016447 Sequence
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32	520	14.2	1563	6 E26332	E26332 Polypeptide
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34	496	13.5	1860	5 CHK11AR	M81846 Gallus gall
35	495	13.5	2314	6 AR179671	AR179671 Sequence
36	495	13.5	2681	9 AF077346	AF077346 Homo sapi
37	491.5	13.4	3090	4 AB020338	AB020338 Equus cab
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42	484.5	13.2	1782	6 AR120235	AR120235 Sequence
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45	482	13.1	4989	10 MUSST2L	D13695 Mus musculu

RESULT 1

ALIGNMENTS

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 LOCUS AB006537 4724 bp mRNA linear PRI 09-Apr-1998
 DEFINITION Homo sapiens mRNA for interleukin 1 receptor accessory protein.
 ACCESSION AB006537
 VERSION AB006537.1 GI:3041772
 KEYWORDS interleukin 1 receptor accessory protein.
 SOURCE Homo sapiens fetal brain cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Saito, T. and Seki, N.
 TITLE Molecular cloning of human interleukin 1 receptor accessory protein
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4724)
 AUTHORS Saito, T.
 TITLE Direct Submission
 JOURNAL Submitted (12-AUG-1997) Toshiyuki Saito, National Institute of
 Radiological Sciences, Genome Research Group, Anagawa 4-9-1, Inage,
 Chiba 263, Japan (E-mail: t_saito@nirs.go.jp, Tel.043-206-3135,
 Fax:043-251-9818)

TURES
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 LKNV"

polya_site
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BASE COUNT 1422 a 902 c 902 g 1498 t
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 Percent Similarity: 86.84% Conservative: 39
 Best Local Similarity: 80.58% Mismatches: 50
 Query Match: 70.63% Indels: 32
 DB: 9 Gaps: 7

US-10-061-727-2 (1-687) x AB006537 (1-4724)

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QY 21 SerGlnArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGlnAsp 40
 DB 267 TCAGACGCTGCGCATGACTGCGGAGCTGACACCAATGAGGCAATCCAGTCTTGAAGAT 326

QY 41 GlnProIlaArgIleLeuValCysProLeuPheGlnHisPheLeuValPheAsnTyrSerThr 60
 DB 327 GAGCCAGCTGCATCAAGTCCACTTTTGACACACTTCTGAATTCACACTACAGACA 386

QY 61 AlHisSerAlaGlyLeuThrLeuIleTrpTyrTyrThrArgGlnAspArgAspLeuGln 80
 DB 617 GATTAATCACTCCGCTGCTGAGATGTTTGAGATGATGATTTGATACAGCTGTCATCTTT 1526

DB 387 GCCCATTCAGCTGACCTTACTGATCTGGTATTGGACTAGCAGGACCGGACCTTGGAG 446
 QY 81 GlnProIleAsnPheArgLeuProGlnAsnArgIleSerIleGlnIleAspValIleLeuTrp 100
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QY 101 PheArgProThrLeuLeuAsnAspThrGlnIleAsnTyrThrCysMetLeuArgAsnThrThr 120
 DB 507 TTCCGCGCCACTCTCTCCATAGACACTGGCACTTAATCTGCAATTTAGAAACACTACA 566

QY 121 TyrCysSerIleValIlePheProLeuGlnValValGlnIleAspSerCysPheAsnSer 140
 DB 567 TATTGACAGCAAGTTCATCTTCCTTGAAGTTGTCAAAAGACAGCTGTTCAATTCC 626

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 DB 627 CCCATGAACTCCAGTGCATTAACGTATATGAAATATGGCAATTCAGAGATCACTTGT 686

QY 161 ProAsnValAspGlyTyrPheProSerSerValIleProThrIleThrTrpTyrMetGly 180
 DB 687 CCAAAATGATGATGATATTTCTTCAGTGCACCAACCACTATCACTTGGTATATGGGC 746

QY 181 CysTyrIleValIleGlnAsnPheAsnValIleProGlnGlyMetAsnLeuSerPheLeu 200
 DB 747 TGTATTAATAATACAGAAATTTATATATGTAATACCGAAGTATGAACTTGAATTTCTTC 806

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 DB 807 AATGCCCTTAATTCAAATATATGAAATTAACATGCTGTTTACATATCCAGAAATATGGA 866

QY 221 ArgThrPheHisLeuThrArgThrLeuThrValIleValValGlySerProIleAsnAla 240
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 DB 987 GACCTCAATTCCTCGTACGGTCTATTTTATGTTTCTGATGATTCCTGCAATGAGGTT 1046

QY 281 TrpTrpThrIleAspGlyIleValIleValIleValIleValIleValIleValIleVal 300
 DB 1047 TGGTGGACCAATGATGAAAGAAACCTGATGACATCAATGATGATTCACCATTAACGAA 1106

QY 301 SerIleSerHisSerArgThrGlnAspGlnTrpArgThrGlnIleLeuSerIleValIle 320
 DB 1107 AGTATTAAGTCATATGATGAAACAGAAAGTGAACAGAACTCAGATTTTGAGCATCAAGAAA 1166

QY 321 ValThrSerGlnAspLeuValIleValIleValIleValIleValIleValIleValIle 340
 DB 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCAATGATGAAAGTCCAAAGCGCAA 1226

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 DB 1227 GTTGCCTAAGCGCCCAAGGTAAGGAGAAAGTGCAGCTCCAAAGATACAGATGGAACG 1286

QY 361 AlaCysGlyPheGlyValIleThrValIleLeuValIleLeuIleValIleValIleVal 380
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QY 421 ValLeuLeuThrLeuArgGlyValIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 440
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 DB 1647 CTGAGAGCTCAAGGCTGACCTA-----GAAATATGAGCTCTCCGGGCACATCAAC 1697
 QY 497 LeuLeuValGlnTyrArgProLeuGlnHisProHisProGlyIleLeuGlnLeuLys 516
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 DB 1752 AGGAGCTAAGACGGTCTCAGCGTCAATTAATGAAAGGGAATAATCCAATATCCACAG 1811
 QY 534 SerLysPheThrLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
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 ARI6115 1740 bp DNA linear PAT 17-OCT-2001
 LOCUS ARI6115 Sequence 1 from patent US 6280955.
 DEFINITION ARI6115
 ACCESSION ARI6115.1 GI:16241289
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1740)
 AUTHORS Cao, Z.
 TITLE Interleukin-1 receptor accessory proteins, nucleic acids and methods
 JOURNAL Patent: US 6280955-A 1 28-AUG-2001;
 FEATURES Location/Qualifiers
 source 1..1740
 BASE COUNT 518 a 360 c 411 g 451 t
 ORIGIN
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 Query Match: 70.48% Indels: 12
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 DB 70 TCAGAAAGCTGCATATACGAGGAGCTAGAACCATATAGGCAATATCCAGAGTTTGAAGAT 129
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 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
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 QY 121 TyrCysSerLysValAlaPheProLeuGlnValValGlnLysAspSerCysPheAsnSer 140
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 QY 141 PrometLysLeuProValHisLysLeuTyrIleGlnTyrGlyIleGlnArgIleThrCys 160
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 QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTyrMetGly 180
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 QY 361 AlaCysGlyPheGlyValAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380

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Qy 421 VALLEULEUTHRIEUAARGIYVALLEUGLUNGLUPHEGLYTYRYSLEUCYSLIPEHE 440
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Db 1390 AGCAGACCCCTCTCGTGTGTTCTTAAGCCCACTAGCTCCAGGAAACCAACCTCTC 1449
Qy 481 LEUGLUPHELYSLEUGLYVALMETCYSGLUNSENSEIIEALATHLYS----- 496
Db 1450 CTGAGAGCTCAAGCTGCGCTA-----GAAATATGCGCTCTCGGGGCAACATCAAC 1500
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Db 1501 GTCATTTTATAGTACGTAACAAGCTGGAAGAAAGCAAG-----GTGAAAGACTGAAG 1554
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RESULT 3
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LOCUS AF029213 Homo sapiens IL-1 receptor accessory protein mRNA, complete cds.
DEFINITION AF029213
ACCESSION AF029213
VERSION AF029213.1 GI:2599126
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1740)
REFERENCE Huang,J., Gao,X., Li,S. and Cao,Z.
AUTHORS Recruitment of IRAK to the interleukin 1 receptor complex requires
TITLE Interleukin 1 receptor accessory protein
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (24), 12829-12832 (1997)
MEDLINE 98058729
PUBMED 9371760
2 (bases 1 to 1740)
REFERENCE Huang,J., Gao,X., Li,S. and Cao,Z.
AUTHORS Direct Submission
TITLE Submitted (07-OCT-1997) Biology, Tularek, Inc., 2 Corporate Dr.,
JOURNAL South San Francisco, CA 94080, USA
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VERSION     X85999.1 GI:887520
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SOURCE     Mus musculus.
ORGANISM   Mus musculus.
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REFERENCE
AUTHORS     Ju, G.W.
TITLE       Submitted (31-MAR-1995) G.W. Ju, Hoffmann-La Roche Inc., 340
            Kingsland Ave., Nutley, NJ 07110, USA
REFERENCE   2 (bases 1 to 3355)
AUTHORS     Greenfeder, S.A., Nunes, P., Kwee, L., Labow, M., Chizzonite, R.A. and
            Ju, G.
TITLE       Molecular cloning and characterization of a second subunit of the
            interleukin 1 receptor complex
JOURNAL     J. Biol. Chem. 270 (23), 13757-13765 (1995)
MEDLINE     95293970
PubMed     7775431

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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE
 1 (bases 1 to 1862)
 AUTHORS
 Liu, C., Chalmers, D., Maki, R. and De Souza, E. B.
 TITLE
 Rat homolog of mouse interleukin-1 receptor accessory protein:
 cloning, localization and modulation studies
 JOURNAL
 J. Neuroimmunol. 66 (1-2), 41-48 (1996)
 MEDLINE
 PUBMED
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 8964912
 REFERENCE
 2 (bases 1 to 1862)
 AUTHORS
 Liu, C.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (06-FEB-1996) Changlu Liu, Molecular Biology, Neuroocrine
 Biosciences, Inc., 3050 Science Park RD, San Diego, CA 92121, USA
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QY      481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
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QY      497 LeuIleValIleGluTyrrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
DB      1594 GTCAATTATGACAGTACAAAGCTGTGAAGAC-----TTGAAAGGTGAAA 1638
QY      517 Glu-----SerValSerPheValSerTrpLysGlyLysSerLys 530
DB      1639 GAGCTGAAGCGGGCTAAAGTCCGTCTACCTCATTAATGAAAGGAGGAAATTCACAG 1698
QY      531 HisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSer 550
DB      1699 TATCTTCAGGCGAGGTTCTGGAAGCAGCTGACAGGTGGCCATGCCAGTGAAGAG----- 1752
QY      551 AlaSerSerGlyTrpAsnGluSer 556

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VERSION BC021159.1 GI:18088147
 KEYWORDS MGC.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1916)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeffrey B. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadeus@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAX Plate: 18 Row: 1 Column: 21
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6680420.

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 DB: 10 Gaps: 0

US-10-061-727-2 (1-687) x BC021159 (1-1916)
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RESULT 9
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 ACCESSION AK095107
 VERSION AK095107.1 GI:21754300
 KEYWORDS oligo capping; f1s (full insert sequence).

SOURCE Homo sapiens hippocampus cDNA to mRNA, clone_1lb:BRHIP2
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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
1 Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
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Yamamoto,U., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
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Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuko,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2226)
AUTHORS Isogai,T. and Yamamoto,U.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FUJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB) (supported by Japan
Construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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QY 450 ThrValAlaValAlaPheAspPheIleGlnArgSerArgMetIleValIleuSer 469
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QY 470 PProAspTYrValThrGluYSerIleSerMetLeuGluPhelylsleuGlyValMetCys 489
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AC108747
LOCUS Homo sapiens 3 BAC RP11-268E23 (Roswell Park Cancer Institute Human
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ACCESSION AC108747
VERSION AC108747.5 GI:21535890
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 46509)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooke,S.L., Amaralungu,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbarta,J., Benton,J., Bimge,K., Blankenburg,K., Bonnin,D.,
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Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
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Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Dayla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Eamhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escoto,M.,
Falls,T., Ferriguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
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Gorell,J.H., Guvera,M., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X.,
Hernandez,J., Hernandez,O., Hodgson,A.J., Hognes,M., Hollaway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulky,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,

Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, U., Li, Z., Lichtenage, O., Lien, C., Liu, J., Liu, W., Louisgied, H., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Oghu, M., Okwundu, G., Oragunye, I., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Pirmas, B., Pu, L., Quiles, M., Ren, Y., Rives, M., Rojebokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, A., Shen, H., Shooshitari, N., Sisson, I., Sodergren, B., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Sytek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G., and Gibbs, R.

TITLE
Direct Submission
unpublished

JOURNAL
2 (bases 1 to 46509)

AUTHORS
Worley, K.C.

TITLE
Direct Submission
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL
3 (bases 1 to 46509)

AUTHORS
Worley, K.C.

TITLE
Direct Submission
Submitted (03-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL
4 (bases 1 to 46509)

AUTHORS
Worley, K.C.

TITLE
Direct Submission
Submitted (21-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL
On Jun 21, 2002 this sequence version replaced gi:21306532.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

FEATURES

SOURCE

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot.html>.

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Percent Similarity: 99.586 Conservative: 1
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Query Match: 34.234 Indels: 0
DB: 9 Gaps: 0
US-10-061-727-2 (1-687) x AC108747 (1-46509)

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DB 22841 GATACAGTGAAGCAGCTTTTATTCATTCACAGAGAGAGATGTTGTTCTG 22900
QY 465 SerProAspTyrValThrGluYserIleSerMetLeuGluPheYsLeuGlyValMet 468
DB 22901 ACCCGTCAGTATGTGACAGAAAGACATCAGATGCTGAGATTAACTGGGTCATG 22960
QY 489 CyGlnAsnSerIleAlaThrYsLeuIleValIleGluTyrArgProLeuGluHisPro 508
22961 TGGCAACATCTCATTCGCCACCAAGCTCATTTGTTGAGTACCGTCCCTTGACACCCG 23020
QY 509 HisProGlyIleLeuGluIleuYsGluSerValSerPheValSerTrpYsGlyGluYs 528
DB 23021 CACCCAGGATTTCTTCAGCTCAAGAGTCTGTCTTTCTTGAGCTGGAGGAGAGAAAG 23080
QY 529 SerYsHisSerGlyYserYsPheTrpYsAlaLeuArgLeuAlaLeuProLeuArgSer 548
DB 23081 TCCAAACATTCGCTCTAAATCTCGAAAGCTTTGGCTGCTCTTCCCTGAGAAAGT 23140
QY 549 LeuSerAlaSerSerGlyTTPAsnGluSerCysSerSerGlnSerAspIleSerIleuAsp 568
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QY 589 AlaAlaGlySerProProAlaProGly***MetSerYsHisArgGlyYsSerSerAla 608
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QY 609 ThrCysArgCysValThrTyrCysGluGlnGluAsnHisLeuArgLeuYsSerArg 628
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DB 23441 TCGAAGATCAATGATACAGAAATGACACAGATTTGAAACCTCTCTCCAGATCTCA 23500
QY 669 AlaLeuAlaLeuHisIlePheThrAspLeuSerAsnAsnAsnAspPheTyrIleu 687
DB 23501 GCCTTGTCTTCATTCATTTACAGCACTTATCCAAATACAGACATTTATATCCCA 23557

RESULT 11
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
REFERENCES
AUTHORS
2 (bases 1 to 58987)
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Anderson,S., Barta,N., Bassien,V., Bloom,T., Boguslavskiy,L.,
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Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L25964
Center clone name: 345_H_5

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NOTE: This record contains 72 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will

* be preserved.

1 724: contig of 724 bp in length

* 725 824: gap of 100 bp in length

* 825 1551: contig of 727 bp in length

* 1552 1651: gap of 100 bp

* 1652 2377: contig of 726 bp in length

* 2378 2477: gap of 100 bp

* 2478 3204: contig of 727 bp in length

* 3205 3304: gap of 100 bp

* 3305 4037: contig of 733 bp in length

* 4038 4137: gap of 100 bp

* 4138 4847: contig of 710 bp in length

* 4848 4947: gap of 100 bp

* 4948 5677: contig of 730 bp in length

* 5678 5777: gap of 100 bp

* 5778 6514: contig of 737 bp in length

* 6515 6614: gap of 100 bp

* 6615 7343: contig of 729 bp in length

* 7344 7443: gap of 100 bp

* 7444 8177: contig of 734 bp in length

* 8178 8277: gap of 100 bp

* 8278 9016: contig of 739 bp in length

* 9017 9116: gap of 100 bp

* 9117 9792: contig of 676 bp in length

* 9793 9892: gap of 100 bp

* 9893 10629: contig of 737 bp in length

* 10630 10729: gap of 100 bp

* 10730 11452: contig of 723 bp in length

* 11453 11552: gap of 100 bp

* 11553 12276: contig of 724 bp in length

* 12277 12376: gap of 100 bp

* 12377 13111: contig of 735 bp in length

* 13112 13211: gap of 100 bp

* 13212 13904: contig of 693 bp in length

* 13905 14004: gap of 100 bp

* 14005 14727: contig of 723 bp in length

* 14728 14827: gap of 100 bp

* 14828 15542: contig of 715 bp in length

* 15543 15642: gap of 100 bp

* 15643 16356: contig of 714 bp in length

* 16357 16456: gap of 100 bp

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* 17157 17256: gap of 100 bp

* 17257 17979: contig of 723 bp in length

* 17980 18079: gap of 100 bp

* 18080 18803: contig of 724 bp in length

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* 19636 19735: gap of 100 bp

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* 20455 20554: gap of 100 bp

* 20555 21277: contig of 723 bp in length

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* 24672 25383: contig of 712 bp in length

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* 31116 31215: gap of 100 bp

* 31216 31947: contig of 732 bp in length

* 31948 32047: gap of 100 bp

* 32048 32769: contig of 722 bp in length

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* 32870 33582: contig of 713 bp in length

* 33583 33682: gap of 100 bp

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* 34408 34507: gap of 100 bp

* 34508 35235: contig of 728 bp in length

* 35236 35335: gap of 100 bp

* 35336 36058: contig of 723 bp in length

* 36059 36158: gap of 100 bp

* 36159 36894: contig of 736 bp in length

* 36895 36994: gap of 100 bp

* 36995 37693: contig of 699 bp in length

* 37694 37793: gap of 100 bp

* 37794 38509: contig of 716 bp in length

* 38510 38609: gap of 100 bp

* 38610 39300: contig of 691 bp in length

* 39301 39400: gap of 100 bp

* 39401 40103: contig of 703 bp in length

* 40104 40203: gap of 100 bp

* 40204 40929: contig of 726 bp in length

* 40930 41029: gap of 100 bp

* 41030 41754: contig of 725 bp in length

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* 43512 44234: contig of 723 bp in length

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* 44335 45060: contig of 726 bp in length

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* 45161 45854: contig of 694 bp in length

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* 46781 47505: contig of 725 bp in length

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* 47606 48321: contig of 716 bp in length

* 48322 48421: gap of 100 bp

* 48422 49134: contig of 713 bp in length

* 49135 49234: gap of 100 bp

* 49235 49978: contig of 744 bp in length

* 49979 50078: gap of 100 bp

* 50079 50806: contig of 728 bp in length

* 50807 50906: gap of 100 bp

* 50907 51628: contig of 722 bp in length

* 51629 51728: gap of 100 bp

* 51729 52453: contig of 725 bp in length

* 52454 52553: gap of 100 bp

* 52554 53282: contig of 729 bp in length

* 53283 53382: gap of 100 bp

* 53383 54104: contig of 722 bp in length

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* 55754 55853: gap of 100 bp

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Alignment Scores:

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Score: 1042.00 Matches: 204

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Best Local Similarity: 87.93% Mismatches: 14

Query Match: 28.40% Indels: 3

DB: 2 Gaps: 2

US-10-061-727-2 (1-687) x AC119283 (1-58987)

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QY 469 SerProAspTyrValThrGluYsSerIleSerMetLeuGluPheYsLeuGluValMet 488
 DB 7268 AGCCCTGACCTATGTCACAGAAAGACATCAGCATGCTGAGTTTAACTGGGTGTATG 7209

QY 489 CysGlnAsnSerIleAlaThrYsLeuIleValValGluTyrArgProLeuGluHisPro 508
 DB 7208 TGCAGAACTCCATTCCTCACTAAGCTCATTTGTGTGGAGTACCGTCCGTTGAGCAACC 7149

QY 509 HisPro-GlyIleLeuGlnLeuYsGluSerValSerPheValSerTyrYsGlyGly 528
 DB 7148 CATCCAGGACATCATCAGCTGAGAGAGTCTGTCTTTTGTAAAGCTGGAAAGGAGAAAA 7089

QY 528 sSerIysHisSerGlySerIysPheTyrPheValAlaLeuArgIleValLeuProLeuArg 548
 DB 7088 GTCCAAACATTCCTGCTCCAGATTCTGAAAGCTTGAGCTTGTCTTCCCTGAGAAAG 7029

QY 548 rLeuSerAlaSerSerGlyTyrAsnGluSerCysSerSerGlnSerAspIleSerLeuAs 568
 DB 7028 TCTGAGCCGACAGTCCGGCTGGAATGAGAGCTCTTCTCACTGACATCATGCTGGA 6969

QY 568 rHisValGlnArgArgSerArgLeuYsGluProGluLeuGlnSerSerGlyArg 588
 DB 6968 TCATGTTTCAG---AGGAGAAAGTGGTTTGAAGAGCCCGGAGAACTCCGAAAGCTCAGAGAG 6912

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QY 628 gAlaGluIleHisAsnGlnProGlnTyrGluThrHisLeuYsAlaProValProGlnG 648
 DB 6791 GGCAGAGATGACACACCATCCCGAGTGGGAAACACACTCTGTAAACCTCTCTCCAAAG 6732

QY 648 userGluThrGlnTyrIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSe 668
 DB 6731 GTCGTAAGTCAAGTGAATCAAAATGACCCGACCCGAA---CCGCTCCCGACATCTC 6675

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RESULT 12
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 LOCUS ARI79668
 DEFINITION Sequence 3 from patent US 6326472.
 ACCESSION ARI79668
 VERSION ARI79668.1 GI:20221223
 KEYWORDS
 SOURCES
 ORGANISM
 Unknown.
 Unclassified.
 1 (bases 1 to 2061)
 AUTHORS Timans,J.C., Debets,J.Eduard,Maria,Antonius., Sana,T.R.,
 TITLE Human receptor proteins: related reagents and methods
 JOURNAL Patent: US 6326472-A 3 04-DEC-2001;
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 Best Local Similarity: 31.93% Mismatches: 244
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US-10-061-727-2 (1-687) x ARI79668 (1-2061)

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QY 20 AlasSerGluArgCysAspAspTyrGluYsAspThrMetArgGlnIleGlnValPheGlu 39
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QY 40 AspGluProAlaArgIleYsCysProLeuPheGluHisPheLeuYsPheAsnTyrSer 59
 DB 136 GGTGAACAGCTCCGAGTGAATGTGCTTCTACAGTTATATTCGTAACCACTATAGC 195

QY 60 ThrAlaHisSerAlaGlyLeuThrLeuIleTyrTyrTyrThrArgGlnAspArgLeu 79
 DB 196 AGGCGCCAGACATCGGCTCAGCTTATGTGTAC-----AAAAACAAGCTGATTTG 249

QY 80 GluGluProIleAsnPheArgLeuProGluAsnArgIleSerIysGluYsAspValLeu 99
 DB 250 GAAGAGCCCATATCTT---TCAGAGTCCAGATATGACAAAGAGAAATTCATTA 303

QY 100 TrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThr 119
 DB 304 TGGTTCACTACGCTGAGGACAAAGACATGATCTTACATTTGTCTTTAAGAACTCA 363

QY 120 ThrTyrCysSerYsValAlaPheProLeuGluValAlaGlnYsAspSer-----Cys 137
 DB 364 ACATATTCGATGAAGTGTCAATGCTTCACTGCTGTCAGAGATGAATACAGGCTGTGC 423

QY 138 PheAsnSerProMetYsLeuProValHisYsLeuTyrIleGluTyrGly----- 154
 DB 424 TACACAGCAGAGATCCG-----TATTTGAAGAAATCTGAAGTCACT 465

QY 155 ---IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValYsPro 173
 DB 466 AAAAAGAAAGATCTTCCTGTCCAGACATGATGATTTAAAAAGTCCATACAGAGCT 525

QY 174 ThrIleThrTyrMetGlyCysTyrYsIleGlnAsnPheAsnValIleProGlu 193
 DB 526 GATGTGTGTGTATTAAGATGCAAGCAAAATGTGAGAAAGCATTAATTAATACAGAA 585

QY 194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213
 DB 586 GGAATATGCTCTGTATCCAGAGATTCAGAAAGAGATGAGAGAAATTAACATGTGA 645

QY 214 ValIleThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValYsVal 233
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QY 234 ValGlySerProYsAsnAlaValPro---ProValIleHisSerProAsnAspHisVal 252
 DB 694 ACAGCTTATACAGACAGACAGCTCCCAAGCCATGTTCCCATGAGATGAGCAAGT 753

QY 253 ValTyrGluYsGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPhe 272
 DB 754 GTTAATAGATGTCACCTGGTGAAGCTTGAACATCCCTCGAAGACATCTTCGATTC 813

QY 273 LeuMetAspSerArgAsnGluValTyrThrThrIleAspGlyYsYsProAspAspIle 292
 DB 814 ACTGAGAGCTCTGGCCCAATGATCTACTGG---ATGAAGAGAGAAAG----- 858

QY 293 ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGlnAspGluThrArg 312
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ACCESSION AJ290436
VERSION  AJ290436.1 GI:7688204
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SOURCE  human.
ORGANISM Homo sapiens
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REFERENCE
  1 Ferrante, M.I., Ghiani, M., Bulfone, A. and Franco, B.
    IL1RAPL2 maps to Xq22 and is specifically expressed in the central
    nervous system
  JOURNAL Gene 275 (2), 217-221 (2001)
  MEDLINE 21472256
  PUBMED  11587848
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  TITLE   Ferrante, M.
  JOURNAL Direct Submission
  Submitted (02-MAY-2000) Ferrante M., Telethon Institute of
  Genetics and Medicine, via Olgettina, 58, 20132 Milano, ITALY
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Pred. No.: 2,676-55 Length: 2080
Score: 825.00 Matches: 228
Percent Similarity: 46.78% Conservative: 106
Best Local Similarity: 31.93% Mismatches: 244
Query Match: 22.49% Indels: 136
DB: Gaps: 27
US-10-061-727-2 (1-687) x HSA290436 (1-2080)
QY 1 MetThrLeuLeuTrpCys---ValValSerLeuTrpPheTyrGlyLeuLeuGlnSerAsp 19
   ::: |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 215 AGGGCCCAAGACAGACGCTGACGCTTATGCTGATC-----AAAAACAAGGTATTTG 268
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Db 269 GAAGAGCCCATCATCTTT-----TCAGAGGTCAGGATGAGCAAGAGAGATTCACATA 322
QY 100 TrpPheArgProThrLeuLeuAsnAspTrpGlyAsnTyrThrCysMetLeuArgAsnThr 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 323 TGGTTCACTACGCTGAGGACCAAGACAGTGAATTTCTACACTTGTTTATAGAAACTCA 382
QY 120 ThrTyrCysSerLysValAlaPheProLeuGluValAlaGlnLysAspSer-----Cys 137
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 383 ACATNTGATGATGAAGTGTGCATATGCTCTTGAAGTGTGACAGAGAAATGATCAGGCTGTGC 442
QY 138 PheAsnSerProMetLysLeuProValHisLysLysLeuTyrIleGluTyrGly----- 154
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 443 TACAACAGCAGGATCCGC-----TATTTGAAATAAATCTGAAGTCACT 484
QY 155 ---IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysPro 173
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



```

Qy 548 -----SerLeuSerAlaSerSergly 554
Db 1868 GCAGACAGAGACTTTTGGAGAACTCCAGCCTATACCCCTTATTTGCCATGACCACTACT 1927
Qy 555 TTPANGIUSERCYSSEISERGILNLSERASPILSERLEUASPHEISVALGILNARGARG 574
Db 1928 TCAGCAGCTCTGTGTCTCATCTCAGGCTGATCTC-----1960
Qy 575 SerArgLeuLysGluProGluLeuGlnSerSer-----586
Db 1961 -----CCTGAATTCCACCCCTTCAGATTCAATGCAATGCAAGGACTGT 2002
Qy 587 -----GluArgAlaAlaGlySerProAlaProGly**MetSer 600
Db 2003 TGCAGAGGTTATTAACATGATACCAACGACGACTTCCAGTACTTCTTAGGCAAC 2062
Qy 601 LysHisArgGlyLysSerSerAlaThrCysArgCysValThrTyrcysgluglyGlu 620
Db 2063 CACCAT-----ACTTATTGTAACTCTGCTGACGCTACTCAACGACAG 2107
Qy 621 AsnHisLeuArgAsn-----LysSerArgAlaGluLeHis 632
Db 2108 CTACCCCTTAATAACACCCCTGAAGATACCCAGGAATTTTCAC 2149

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Search completed: April 30, 2003, 11:50:48
 Job time : 3479 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2003, 09:40:19 ; Search time 275 Seconds

(without alignments)
5625.901 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLLMCVSLYFYGILOSDA.....SALALHHFTDLNNNDPYLL 687

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DBV=xlh
-Q/cgnt_1/USPTO.spool/US10061727/runat.23042003.083115.7882/app.query.fasta.1.839
-DB=N.Geneseq.101002 -QPM=faetap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum40 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTENT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10061727 @CGN 1.1 200 @runat.23042003.083115.7882 -NCPUS=6 -ICPU=3
-NO_XLPHY -NO_MAP -LARGEQUERY -NRG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MAPN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N.Geneseq.101002.*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2586	70.5	1740	23 AAS15608	Human interleukin-
2	2580	70.3	1713	17 AAT32026	Human interleukin-
3	2327.5	63.4	1713	17 AAT32028	Mouse interleukin-
4	2327.5	63.4	3355	23 AAS15609	Mouse interleukin-
5	1934	52.7	1077	17 AAT32027	Soluble interleukin-
6	1930	52.6	2733	21 AAO5048	Fusion polypeptide
7	1889	51.5	2155	19 AAV23659	Human interleukin-
8	825	22.5	2061	20 AAV58245	Human IL-1R08 codi
9	825	22.5	2061	24 AAD27170	Human interleukin-
10	817.5	22.3	1979	20 AAX84308	Human TIGRR codin
11	800	21.8	1737	20 AAX58247	Human IL-1R08 codi
12	800	21.8	1737	24 AAD27169	Human interleukin-
13	772	21.0	2091	21 AAA27919	Human Xrec2 CDNA c
14	772	21.0	3122	22 AAK51941	Human polynucleoti
15	767	20.9	2537	24 AAD27179	Human interleukin-
16	765	20.9	3120	22 ABA09029	Human oligophrenin
17	765	20.9	3120	22 AAK52925	Human polynucleoti
18	531	14.5	287	22 AAI24540	Probe #14473 for g
19	531	14.5	287	22 AAI49786	CDNA encoding a hu
20	528.5	14.4	1620	19 AAV48299	CDNA encoding a hu
21	528.5	14.4	1620	20 AAZ20661	Human interleukin-18 rec
22	528	14.4	1626	18 AAT88774	Human receptor pro
23	528	14.4	1626	20 AAX87651	Human interleukin-
24	528	14.2	1626	20 AAD31175	Human IL-18 recept
25	520	14.2	1563	20 AAZ20655	Interleukin-18 rec
26	495	13.5	2314	20 AAX58241	Human IL-1R09 codi
27	495	13.5	2314	24 AAD27173	Human interleukin-
28	495	13.5	2681	20 AAX87650	Human interleukin-
29	495	13.5	2681	20 AAZ00059	Human ACTL CDNA.
30	495	13.5	2681	24 AAD31174	Human IL-18 recept
31	495	13.5	2356	21 AAA09035	Human TANGO 191 cd
32	488.5	13.3	2356	10 AAN90114	CDNA of murine int
33	488.5	13.3	2356	15 AAO73762	Murine IL-1 recept
34	485.5	13.2	2356	10 AAN90028	CDNA of clone GEMB
35	484.5	13.2	1731	10 AAN90028	Murine interleukin
36	484.5	13.2	1782	15 AAO71902	CDNA encoding mus
37	484.5	13.2	1782	18 AAT45877	Mouse interleukin-
38	484.5	13.2	1782	22 AAC68648	CDNA encoding a mo
39	484.5	13.2	1782	22 AAF24246	Murine interleukin
40	482	13.1	4989	16 AAO85962	Mouse STYL gene.
41	482	13.1	4989	18 AAD03365	DNA encoding trans
42	479.5	13.1	2830	18 AAT88775	Mouse receptor pro
43	479.5	13.1	2830	20 AAX87653	Mouse interleukin-
44	478	13.0	1557	19 AAV48294	CDNA encoding a mu
45	478	13.0	1557	20 AAZ20656	Interleukin-18 rec

ALIGNMENTS

RESULT 1	AAS15608	standard; CDNA, 1740 BP.
ID	AAS15608	
XX		
AC	AAS15608;	
XX		
DT	21-MAY-2002	(first entry)
XX		
DE	Human interleukin-1 Receptor accessory protein (IL-1R acp) CDNA.	
XX		
KW	IL-1R acp; human; interleukin-1 receptor accessory protein; NF-kappaB;	
KW	IL-1; IL-1R; ss; inflammatory response.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	10..1722	
CDS	/*tag= a	
FT		

/product= "IL-1 Receptor accessory protein"

FT
XX
PN
XX
XX
PD
XX
XX
PF
XX
PR
XX
PA
PI
XX
XX
DR
DR
PT
PT
XX
PS

US6280955-B1.
28-AUG-2001.
16-DEC-1997; 97US-0991944.
16-DEC-1997; 97US-0991944.
(TULA-) TULARIK INC.
Cao Z;
MPI; 2001-595441/67.
P-PSDB; AAU09966.
Isolated polypeptide designated interleukin receptor accessory polypeptide is useful for regulating cell function
Claim 11; Fig 2; 21pp; English.

This sequence represents the human interleukin-1 receptor accessory protein (IL-1RACP) cDNA of the invention. The interleukin receptor accessory protein (IL-1RACP) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either IL-1RI or IL-1RACP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-1RI and IL-1RACP as a result of protein overexpression can elicit a signaling pathway leading to NF-kappaB activation. Modulation of signal transduction involving NF-kappaB in a cell may be achieved by modulating the activity of IL-1RACP using binding agents such as agonists and antagonists. Hybridization probes to the cDNA sequence can be used to identify wild-type and mutant IL-1RACP alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In therapy, therapeutic IL-1RACP nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active IL-1RACP. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor accessory polypeptide (IL-1RACP) to a binding target.

Sequence 1740 BP; 518 A; 360 C; 411 G; 451 T; 0 other;

Alignment Scores:

Ref. No.: 3 73e-214 Length: 1740
Percent Similarity: 2586.00 Matches: 488
Best Local Similarity: 91.43% Conserves: 35
Query Match: 85.31% Mismatches: 37
DB: 70.48% Indels: 12
Gaps: 4

US-10-061-727-2 (1-687) x AAS15608 (1-1740)

QY 1 MetThrIleuLeuTrpCysValaIserLeuTyrrhPheTyrGlyIleLeuGlnSerAspAla 20
DB 10 ATGACACTTCCTGTCGTGTGTAGTGTCTCTACTTTATGGAATCTTGCAAGTGAATGCC 69
QY 21 SerGluArgCysAspAspTTPGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 70 TCGAAGAGCTGCGAGTCTGGGACCTAGACACCAATGAGCAAAATCAAGTGTGAAGAT 129
QY 41 GluProIleArgIleLeuTyrCysProLeuPheGlnIleIlePheLeuLysPheAsnTyrSerThr 60
DB 130 GAGCAGACTGCATCAAGTCCCACTTTGAAACACTTTGAAATTCACCTAGGACCA 189
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTyrTrpThrArgGlnAspArgAspLeuGlu 80
DB 190 GCCCATTCACCTGGCTTACTCTGATCTGTATGACTAGGACGACCGGACCTTGAG 249

QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerTyrGlyLeuAspValIleuTrp 100
DB 250 GAGCCAAATTAACCTCCGCTCCCGAGAACCCGATTAATGTAAGAGAAATGCTGTGG 309
QY 101 PheArgProThrIleLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB 310 TTCGGGCCCACTCTCTCTCATAGCACTGGCACTATACCTGATGTTAAGAAACATCA 369
QY 121 TyrCysSerTyrValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
DB 370 TATTCAGCAAAAGTTGCATTTCCCTTGGAAAGTGTTCAAAGACAGCTGTTCATATCC 429
QY 141 ProMetTyrLeuLeuProValAlaHisTyrLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB 430 CCCATGAAACTCCCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 489
QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTyrMetGly 180
DB 490 CCAATGTATGATGATGATATTTCTTCCAGTGCATTAACCACTATCATCTGATATGGGC 549
QY 181 CysTyrTyrIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB 550 TGTATTAATAATACAGAAATTTAATAATTAATAATTAATAATTAATAATTAATTAATTA 609
QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValIleThrTyrProGluAsnGly 220
DB 610 ATTCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 669
QY 221 ArgThrPheHisIleuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
DB 670 CTTACCTTTCATCTCAACGAGCTCTGATGTAAGTGTAGTGGCTCTCCAAAATATGCA 729
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
DB 730 GTGCCCTCTGTATCATCATCACTATGATGATGATGATGATGATGATGATGATGATGAT 789
QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
DB 790 GAGCTAATCAATTCCTGTAACGCTGTATTTTATTTTATTTTATTTTATTTTATTTTAT 849
QY 281 TrpTrpThrIleAspGlyLysLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
DB 850 TGTGTGACATTTGATGAGAAAAAACCCTGATGACATCATTTGATGATGCCATTAAACGA 909
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB 910 AGTATTAATCATATGATAGAACAGAAATGAAACAGAACTCAGATTTTGACATCAAGAAA 969
QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaLysSerAlaLysGlyGlu 340
DB 970 GTTACCTCTGAGAGATCTCAAGCGCAGCTATGCTGTCAAGCTAGAGAGTCCAAAGCGGAA 1029
QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
DB 1030 GTTGCCTAAGCAGCCAAAGGTGAAGCAAGAAAGTCCAGCTCCAAAGTACAGATGAACTG 1089
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValIleValIleVal 380
DB 1090 GCTTGAGTTTGGAGCCACAGTCCGTAGTGATGATCTCATTTGTTTGTATACCATGTT 1149
QY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
DB 1150 TACTGCTAGAGATGATGCTCTATTTTATCCGGCTCATTTTGGAAACAGATGAACCATTTTA 1209
QY 401 AspGlyLysGlyTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
DB 1210 GATGAAAAAGATATGATATTTATATCTATCTATGCAAGAAATCCGGAAGAAAGAAATTT 1269
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrTyrLysLeuCysIlePhe 440
DB 1270 GTATTAATCAACCTCCGTGAGATTTTGGAGATGAATTTGGATACAGAGTGTGATCTTT 1329

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Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGlnAlaValPheAspPheIleGlnArg 460
Db 1330 GACCGAGACAGCTGCTGGCGGGAATGTCACAGATGAGACTTGAAGCTTCATTGAGAAA 1389
Qy 461 SerArgArgMetIleValIleLeuSerProAspTyrValThrGlnLysSerIleSerMet 480
Db 1390 ACCAGACGGCTCTGTTGTTTCTTAAGCCCACTAGCTGCTCCAGGAAACCAAGCCCTC 1449
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
Db 1450 CTGGAGCTCAAGGCTGGCTA-----GAAATATGCTCTCTCGGGCAACATCAAC 1500
Qy 497 LeuIleValIleGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
Db 1501 GTCATTATTAAGTACAGTACAAAGCTGGAAGAAACGAG-----GTGAAGAAGCTGAAG 1554
Qy 517 GluSer-----ValSerPheValSerTyrPheGlyGlyLysSerLysHisSerGly 533
Db 1555 AGGGCTAAGACGGTCTCAAGCTCAATTAATGAAAGGGAAGAAATCCAAATGATCCACAG 1614
Qy 534 SerLysPheThrLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
Db 1615 GCGAGGTTCTGAGAGCAGCTGCGAGTGGCCATCCAGTGAAGAAAGTCCCAAGCGGCTCT 1674
Qy 554 GlyTyrAsnGluSerCysSerSerGlnSerAspIle 565
Db 1675 AGCAGTATGATGACGAGGCGCTCTGTTATCATCTTTG 1710

RESULT 2
AAT32026
ID AAT32026 standard; cDNA, 1713 BP.
AC AAT32026;
XX
XX 14-OCT-1996 (first entry)
XX
XX Human interleukin-1 receptor accessory protein cDNA.
XX
XX Interleukin-1 receptor accessory protein; IL-1 antagonist;
XX inflammation; therapy; antiinflammatory; ss.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX sig_peptide 1..60 a
XX mat_peptide 61..1710
XX /*tag= b

WO9623067-A1.
PD 01-AUG-1996.
PF 17-JAN-1996; 96WO-EP00181.
PR 23-JAN-1995; 95US-0376268.
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PI Chizzone RA, Ju GW;
XX
XX MPI. 1996-162691/36.
XX P-PSDB; AAM01911.
XX
XX Isolated interleukin-1 receptor accessory protein - used to develop
XX of interleukin-1
XX
XX Claim 2; Page 71-72; 115pp; English.
XX
XX A cDNA clone (AAT32026) codes for human interleukin-1 receptor
XX accessory protein (IL-1R Acp), a protein that inhibits the
XX ability of IL-1 to bind to or otherwise activate the IL-1R,

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CC esp. the Type 1 IL-1R. It was obtd. from a human YT cell cDNA
CC library using a probe derived from a human partial genomic clone.
CC The cDNA can be used for the prodn. of pure IL-1R Acp by expression
CC in a host cell. The IL-1R Acp is used to treat or prevent the
CC inflammatory or immunological activities of IL-1.
XX
XX Sequence 1713 BP; 502 A; 358 C; 405 G; 448 T; 0 other;
XX
Alignment Scores:
Pred. No.: 1,216-213 Length: 1713
Score: 2580.00 Matches: 487
Percent Similarity: 91.04% Conservative: 31
Best Local Similarity: 85.59% Mismatches: 45
Query Match: 70.32% Indels: 6
DB: 17 Gaps: 3

US-10-061-727-2 (1-687) x AAT32026 (1-1713)
Qy 1 MetThrLeuLeuTyrCysValIleSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20.
Db 1 ATGACACCTTCTGTTGTTGTTAGTGTAGTCTTCTTATGAAATCTTGCAAGTATGCC 60
Qy 21 SerGluArgCysAspAspTyrPheLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAAAGCTGGGATGATCAGGGAGCTAGACACCATGAGGCAATCCAACTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLeuCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTGGATCAAGTCCCACTTTGAACTTTTAAATTCATCACTACAGCA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuLeuIleTyrTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGTGGCTTATCTGATCTGATCTGATTTGGAAGTATGAGCAAGGACCGGACCTTGA 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
Db 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCCCATTAATGTAAGAAATGCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCCGGCCCACTCTCTCAATACACCTGGCAACTATCACTGATGTAAGAACACTTAC 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValIleGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGACGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAGACAGCTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAGCTCCAGTGCATAACTGTATATGAAATGCGCATTCAGAGATCACTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrThrMetGly 180
Db 481 CCAAAATGATGATGATATTTCTTCCAGTGTCAACCAAGCATATCACTTGGTATATGAGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATTAATAATACAGAAATTTATATATATATATATATATATATATATATATATATATAT 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValIleThrTyrProGluAsnGly 220
Db 601 ATTGCTTAATTTCAATATATATATATATATATATATATATATATATATATATATATATAT 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValIleGlySerProLysAsnAla 240
Db 661 CGTACGTTTCATCTCCAGGACTGCTGATGTAAGTATGAGTGGCTCTCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValIleValTyrGlyLysGluProGlyGlu 260
Db 721 GTCCCCCTGTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTATTCCTCGTACGCTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 840

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QY 281 TTTTTPThrlleaspglylylsyProaspasilleThrlleaspyalThrlleasngu 300
DB 841 TGGGGACCACTATATGAAAAAACTGATGACATCACTATATGATGACACCATTAACGAA 900
QY 301 SerIleSerHisSerArgThrGluaspGluThrArgThrGlnIleuSerIleuSyls 320
DB 901 AGRTAAGTATATGTAGAACAGAAAGATGAAACAAAGAACTGAGTTTGACATCAAGAAA 960
QY 321 ValThrSerGluaspLeuValysArgSerTyrValCysHisAlaArgSerAlaValSylGlu 340
DB 961 GTTACCTCTAGGATCTCAAGCCAGCTATGTCATCTAGTCAAGTGCAGAAAGCGGAA 1020
QY 341 ValAlaValAlaValAlaValSylValSylGlnValAlaProAlaProArgTyrThrValGluLeu 360
DB 1021 GTTGCCAAAGCCAGCCAGGACGAGCAAGAAAGTCCAGACTCCAGATACACAGTGGAACTG 1080
QY 361 AlaCysGlyPheGlyAlaThrValIleuValValIleuIleValValTyrHisVal 380
DB 1081 GCTTGTGTTTGGAGCCAGATCTCTGCTAGTGTGATTTCTCATGTGTTTACCATGTT 1140
QY 381 TTTTTPleuGluMetValleuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
DB 1141 TACTGGCTAGATGATGCTCATATTTTACCGGGCTCATTTTGGAAACAGTAAACCATTTTA 1200
QY 401 AspGlyValGluTyrAspIleTyrValSerTyrAlaArgAlaGluGluGluGluPhe 420
DB 1201 GATGGAAAAAGATATATTTATTTATGATCTTATGCAAGAAATCGGAGAAAGAAATTT 1260
QY 421 ValIleuThrIleuArgGlyValIleuGluAsnGluPheGlyTyrIleuSylPhe 440
DB 1261 GTTTTACTGACCTCTCCGTGAGATTTTGGACAAATGAAATTTGATACAGCTGTGATCTTT 1320
QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
DB 1321 GACCGAGACAGTCTGCTCGGGGGAATGTACAGATGACATTTGAGCTTCATTCAGAAA 1380
QY 461 SerArgArgMetIleValValIleuSerProAspTyrValThrGluValSerIleSerMet 480
DB 1381 AGGAGACGCTCTGCTGTGTTCTTAAGCCCAACTGACCTGCTCCAGGGAAACCCAGCCCTC 1440
QY 481 LeuGluPheIleuGlyValIleuMetCysGlnAsnSerIleAlaThr--LysLeuIleVal 499
DB 1441 CTGGAGCTCAAGGCTGCTGCAAGAAATATGGCTCTCTGGGGCAACATCAACGTCATTTTA 1500
QY 500 ValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnIleuValSylSer 518
DB 1501 GTACAGTACAAAGCTGGAAGAAAGCAAG-----GTAAAGAGCTGGAAGAGGGCTAAG 1554
QY 519 -----ValSerPheValSerTyrPheGlyGlyValSylSerIleSerGlySerLysPhe 536
DB 1555 ACGGTGCTCAGCTCATTAATATGAAAGGGAATAATCCAAAGATATCCACAGGGCAGGTTTC 1614
QY 537 TTPlyAlaLeuArgLeuAlaLeuProLeuArgSerIleuSerAlaSerSerGlyTyrAsn 556
DB 1615 TGGAAAGAGCTGCAAGGCGCATATCCCAAGAAAGTCCCAAGGCGGTCTTACAGATGAT 1674
QY 557 GluSerCysSerSerGlnSerAspIle 565
DB 1675 GAGCAGGCGCTCTCGTATTCATCTTTG 1701

```

RESULT 3

AAT32028
ID AAT32028 standard; cDNA; 1713 BP.

AC AAT32028;
XX 14-OCT-1996 (first entry)
DE Mouse interleukin-1 receptor accessory protein cDNA.
XX Interleukin-1 receptor accessory protein; IL-1 antagonist;
KM Inflammation; therapy; antiinflammatory; ss.
KV

```

XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT sig_peptide 1..60
XX FT mat_peptide /*tag= a 61..1710
XX FT /*tag= b
XX PN W09623067-A1.
XX PD 01-AUG-1996.
XX PF 17-JAN-1996; 96MO-EP00181.
XX PR 23-JAN-1995; 95US-0376268.
XX PA (HOF) HOFMANN LA ROCHE & CO AG F.
XX PI Chizomite RA, Ju GW;
XX DR WPI; 1996-362691/36.
XX DR P-PSDB; AAM01913.
XX PT Isolated interleukin-1 receptor accessory protein - used to develop
XX PT prods. to treat or prevent inflammatory or immunological activities
XX PS of interleukin-1
XX PS Example 7; Page 76-77; 115pp; English.
XX CC A cDNA clone (AAT32028) codes for mouse interleukin-1 receptor
XX CC accessory protein (IL-1R AcP), a protein that inhibits the
XX CC ability of IL-1 to bind to, or otherwise activate, the IL-1R.
XX CC esp. the Type 1 IL-1R. It was obt. by screening cell-surface
XX CC proteins in COS-7 cells transfected by 373-L1 cDNA using
XX CC anti-murine IL-1R AcP monoclonal antibody 4C5, and isolation of
XX CC cDNA clones from positive lines. The murine cDNA was used to
XX CC obtain a partial genomic clone of the human homologue. A probe
XX CC derived from this genomic clone was then used to isolate the
XX CC full-length cDNA (AAT32026) for human IL-1R AcP (AAM01911).
XX SQ
XX Sequence 1713 BP; 473 A; 366 C; 428 G; 426 T; 0 other;
XX Alignment Scores:
XX Pred. No.: 9,17e-192 Length: 1713
XX Score: 2327.50 Matches: 429
XX Percent Similarity: 87.61% Conservative: 66
XX Best Local Similarity: 75.93% Mismatches: 55
XX Query Match: 63.44% Indels: 15
XX DB: 17 Gaps: 5

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US-10-061-727-2 (1-687) x AAT32028 (1-1713)

```

QY 1 MetThrIleuLeuTyrCysValAlaSerLeuTyrPheTyrGlyIleuGlnSerAspAla 20
DB 1 ATGGGACCTTCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 21 SerGluArgCysAspAspTyrGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCGGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 41 GluProAlaArgIleLeuGlyCysProLeuPheGluHisPheLeuIlePheLeuSerThr 60
DB 121 GAGCTGGCTGATCAATCAAGGCGCCCTTTTGAACATCTTCTTAAGTACAACTACAGACT 180
QY 61 AlaHisSerAlaGlyLeuThrIleuIleTyrTyrThrArgGlnAspArgAspLeuGln 80
DB 181 GCCCATTTCTCTGCGCTTACCTGATCTGTACTGACCAAGCCAGAACCCGGAACCTGAG 240
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
DB 241 GAGCCATTAACCTTCGCGCTCCAGAGATCCATCATGATGAGAAAGATGTGCTCTGG 300

```

QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
 DB 301 TTCGGGCCCCCTCTCTCATATGACACGGGCAATTAACCTGATGTTGAGAACACAACT 360
 QY 121 TyrCysSerIleValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
 DB 361 TACTGGACGAAGATTCATTTCCCTGGAGGTGTTCAGAAAGACAGCTGTTCATTTCT 420
 QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrIleGlnArgIleThrCys 160
 DB 421 GCCATGAGATTCCTCAGTGCACAAAGATGATATGAAATGGCATTCATTAAGATCACTG 480
 QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly 180
 DB 481 CCAATAGTGAACGATTAATCTTCTCCAGTGCACAAACATCGGTCACTTGATTAAGGAT 540
 QY 181 CysTyrLysIleGlnAsnProLeuAsnValIleProGluGlyMetLysLeuSerPheLeu 200
 DB 541 TGTACTGAATATGATGACCTTTCATTAATGTACTACCGAGGGCATGAACTTGACCTTTTTC 600
 QY 201 IleAlaLeuIleSerAsnGlnLysAsnTyrThrCysValValThrTyrProGluAsnGly 220
 DB 601 ATCCCTTGTGTTCAATATACGAAATTAACATGATGTTGATACATATCTGTAAGACGGA 660
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 DB 661 CGTCTCTTCACTGCACAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
 DB 721 TTGCCACCCAGATCTATTTCTCAAAATGACCGGTGTCTATATGAAAGAACCAAGAGAG 780
 QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
 DB 781 GAACTGTTATTCCTCGCAAGTCTATTTCAATTAATGATGATGATGATGATGATGATGAT 840
 QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 DB 841 TGTGTGACCATTCATGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 900
 QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
 DB 901 AGGTGAATGTTATTTCTCAACCGAAGATGAAACAAAGACCTCAGATTTTGGACATCAAGAA 960
 QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGluGlu 340
 DB 961 GTCACCCCGAGATCTCAGCGCAACTATGTCATGCTGCAATATCCAAAGGAGGAGAA 1020
 QY 341 ValAlaValAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
 DB 1021 GCTGACAGAGCTGCCAAGTGAAGAAAGAAAGTATACCAACCAAGTACACAGTACAACTC 1080
 QY 361 AlaCysGlyPheGluValAlaThrValLeuLeuValIleLeuIleValValTyrHisVal 380
 DB 1081 GCGTGTGTTTGGACCGACGCTTTCGTGTAGTGTTCATTTGTTGTTTACATGTTT 1140
 QY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
 DB 1141 TACTGCTGAGATGATGCTCTTTTACCAAGCTCCTTGGAAACAATGAAACAATTTCT 1200
 QY 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluGluPhe 420
 DB 1201 GATGAAAGAGATATATTTATGTTTCTATGCAAGAAATGAGAAAGAAAGAAATTT 1260
 QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
 DB 1261 GTGCTGCTACCGCTGCTGAGATTTTGGAGAAATGAGATTTGAGATTAACAAGCTGCTCAT 1320
 QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
 DB 1321 GACAGAGACAGCTGCTGCTGAGGAGAAATTTGACAGAGTGAAGACCTTGAAGCTTCATGAAA 1380
 QY 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480

DB 1381 AGCAGACGACTCTGTTTCTTAAGTCCCACTAGTCTCCAGGAAACAAAGCCCTC 1440
 QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
 DB 1441 CTGAGCTCAAGCTGGCTTA-----GAAATATAGCTCTCCGGGCAACATCAAC 1491
 QY 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyLysLeuGlnLeuLys 516
 DB 1492 GTCATTTTATGTCAGTACAAAGCTGTAAGAGCATGAG-----GTGAAAGAGCTGAAG 1545
 QY 517 GluSer-----ValSerPheValSerTyrPheGlyGlyLysSerLysHisSerGly 533
 DB 1546 CCGGCTAAGACCGTCTCAGCTCAATTAATGAAAGAGAGAAATCAAGTATCTCTCAG 1605
 QY 534 SerLysPheTrpLysValAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerLys 553
 DB 1606 GGCAGGTTCTGAAAGCATGTGACGTCATGCCAGTGAAGAG-----AGTCCC 1656
 QY 554 GlyTyrPasnGluSer 558
 DB 1657 AGTGTGTTAGCAAT 1671
 RESULT 4
 AAS15609
 ID AAS15609 standard; cDNA; 3355 BP.
 AC AAS15609;
 XX
 XX 21-MAY-2002 (first entry)
 DT
 XX
 DE Mouse interleukin-1 Receptor accessory protein (IL-1R ACP) cDNA.
 XX
 XX IL-1R ACP; mouse; interleukin-1 receptor accessory protein; NF-kappaB;
 KM IL-1; IL-1RI; ss; inflammatory response.
 OS Mus sp.
 PH
 FT Key Location/Qualifiers
 FT CDS 135..1847
 FT /*tag= a
 FT /product= "Interleukin-1 receptor accessory protein"
 PN
 XX US6280955-B1.
 PD 28-AUG-2001.
 XX
 PF 16-DEC-1997; 97US-0991944.
 XX
 PR 16-DEC-1997; 97US-0991944.
 XX
 PA (TULAR) TULARIK INC.
 XX
 PI Cao Z;
 XX
 DR MPI: 2001-595441/67.
 DR P-PSDB; AAU09967.
 XX
 PT Isolated polypeptide designated interleukin receptor accessory
 XX polypeptide is useful for regulating cell function
 PS Example: Fig 2; 21pp: English.
 CC This sequence represents the mouse interleukin-1 receptor accessory
 CC protein (IL-1R ACP) cDNA that was used to generate a cDNA fragment
 CC used as a hybridisation probe to isolate, from a cDNA library,
 CC the human IL-1R ACP cDNA of the invention. The interleukin receptor
 CC accessory protein (IL-1R ACP) and its modulators (agonists/antagonists)
 CC are useful for regulating cell function. Transient expression of either
 CC IL-1RI or IL-1RAcP alone does not result in ligand-independent induction
 CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
 CC coexpression of both proteins resulted in a 20-fold increase in
 CC activation of NF-kappaB activity to a level comparable to that induced

CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1R ACP as
CC a result of protein overexpression can elicit a signaling pathway
CC leading to NF-kappaB activation. Modulating signal transduction
CC involving NF-kappaB in a cell may be achieved by modulating the activity
CC of IL-1R using binding agents such as agonists and antagonists.
CC Hybridisation probes to the cDNA sequence can be used to identify wild-
CC type and mutant IL-1R ACP alleles in clinical and laboratory
CC samples. Mutant alleles are used to generate allele-specific
CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
CC of diseases or disorders with an inflammatory response. In
CC therapy, therapeutic IL-1RACP nucleic acids are used to modulate
CC cellular expression or intracellular concentration or availability of
CC active IL-1R ACP. This invention also comprises a method of screening for
CC an agent that modulates the interaction of an interleukin receptor
CC accessory polypeptide (IL-1R ACP) to a binding target.

XX Sequence 3355 BP; 909 A; 742 C; 753 G; 951 T; 0 other;

Alignment Scores:

Pred. No.:	2,45e-191	Length:	3355
Score:	2327.50	Matches:	443
Percent Similarity:	83.36%	Conservative:	73
Local Similarity:	71.57%	Mismatches:	76
Match:	63.44%	Indels:	28
DB:	23	Gaps:	8

US-10-061-727-2 (1-687) x AAS15609 (1-3355)

QY 1 MetThrIleuLeuTrpCysValValSerIleuTrpPheTyrglyIleuGlnSerAspAla 20
DB 135 ATGGAGATTCTGTGGTATTGATGATGCTGTCTCTTAAGGATCTCGAGAGTCAATGCT 194
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 195 TCGGAGCGCTGTGATGCTGGGACTAGTACATGCAATGCTCAATGCTTTTAAAGT 254
QY 41 GluProAlaArgIleLeuCysProIleuPheGlnIlePheLeuLysPheAsnTrpSerThr 60
DB 255 GAGCGGCTCGAATCAAGTGGCCCTCTTGAACCTCTTGAAGTACCACTACAGCACT 314
QY 61 AlaHisSerAlaGlyLeuLeuThrIleuLeuTrpTyrglyIleuArgGlnAspArgAspLeuGln 80
DB 315 GCCATTCTCTGGCTTACCTGATCTGTGACTGGACCAAGCAAGCAAGCAAGCTGGAG 374
QY 81 GluProIleuAsnPheArgLeuProGluAsnArgIleSerGlyLeuLysAspValLeuTrp 100
DB 375 GAGCCCATTAATCTTCCGCTCCAGAGATCCATCATAGAGAGCAAGATGCTGCTGG 434
QY 101 PheArgProThrIleuLeuAsnAspThrGlyAsnTrpTyrglyIleuArgGlnAspThrThr 120
DB 435 TTCGGGCCACCTCTCTCAATACAGGCAATTAACCTGCAATGTTGAGAACCAACT 494
QY 121 TyrCysSerIleuValAlaPheProIleuGlnValIleGlnLysAspSerCysPheAsnSer 140
DB 495 TACTGACAGAAAGTTGATTCCTCCGGAAGTTGTTCAAGAGACAGCTGTTCAATTC 554
QY 141 ProMetLysLeuProValHisLysLeuTrpIleGlyIleuArgIleuThrCys 160
DB 555 GCCAGGAAATTCACAGTGCACAGAGATGATTAATTAAGCAATTCATCAATTC 614
QY 161 ProAsnValAspGlyTyrglyPheProSerSerValLysProThrIleuThrTrpIleuMetGly 180
DB 615 CCAATGTAGAGCGATCTTCTCTCAATGCAATCAATCGGTCACTTGGTATTAAGGT 674
QY 181 CysTyrglyIleuGlnAsnPheAsnValIleProGluGlyMetAsnLysSerPheLeu 200
DB 675 TGTACTGAATAGTGACATTCTCATATGATTAATCAACGAGGACATGAATCTTATTC 734
QY 201 IleAlaIleuIleSerAsnAsnGlyLeuTrpTyrglyIleuValValThrTyrglyLeuGln 220
DB 735 ATCCCTTGTGTTCAAAATTAAGCAATTAATCAATGTTGTTCAATTAATCTTAAAGCA 794
QY 221 ArgThrPheHisIleuThrArgThrIleuThrValValIleGlySerProLysAsnAla 240

DB 795 CGTCTCTTACACCTCACAGAGACTGATGAAGGTGGTGGCTCACAAAGAGTCA 854
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrglyLysGluProGlyGlu 260
DB 855 TTGCGACCCCAAGATCTTCTCCAAATGACCGTGTGTCTATGAGAAAGAACCGAGAG 914
QY 261 GluLeuLeuIleProCysThrValTyrglyPheSerPheLeuMetAspSerArgAsnGlyVal 280
DB 915 GAATGCTTATTCCTTCCAAAGTATTAATTCATTTATGACTCCCAATGAGGTC 974
QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
DB 975 TGTGAGCAATTAATGAGAAAGACCTGATGACGTCAACGACATCACTAATTAAGAA 1034
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB 1035 AGTGAAGTATTAATCTTCAACGAGAGATGAACAGAGACTGATTTGAGCATCAAGAA 1094
QY 321 ValThrSerGluAspLeuLysArgSerTyrglyCysHisAlaArgSerAlaLysGlyGlu 340
DB 1095 GTCAACCCGAGAGATCTGAGCGCACTATGTCTGATGCTGAAATACCAAGGGGAA 1154
QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrglyValGluLeu 360
DB 1155 GCTGAGCAGGCTGCCAAGGTGAACAGAAAGTCAACCAAGTACAGTGAATC 1214
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValIleuIleuValIleuValTyrglyHisVal 380
DB 1215 GCGTGTGTTTGAAGCAGCGCTCTTCTGTGATGCTGATTCATTTGCTTACCATGTT 1274
QY 381 TyrTrpLeuGluMetValLeuPheTyrglyAlaHisPheGlyThrAspGluThrIleu 400
DB 1275 TACGGCTGAGATGCTCTTCTTACAGCTCACTTGGAAAGATGAACAAATCTT 1334
QY 401 AspGlyLysGluTyrglyAspIleTyrglyValSerTyrglyAlaArgAsnAlaGluGluGluPhe 420
DB 1335 GATGGAAGAGATGATTAATTAATTAATGTTTCCATCAAGAAATGGAAGAAAGAAATTT 1394
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrglyLysCysIlePhe 440
DB 1395 GTGCTGCTGAGCGCTGCGTGGAGTTTGGAGATGATGTTGGATCAAGCTGTGATCTTC 1454
QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGlnAlaValPheAspPheIleGlnArg 460
DB 1455 GACAGAGACACCTGCTGGGGGAATTCACATATGACATGACCTGAGCTTATTCAGAA 1514
QY 461 SerArgArgMetIleValIleuSerProAspTyrglyValThrGlyLysSerIleSerMet 480
DB 1515 AGCAGAGACCTCGTGTGCTTCTTAAGTCCCACTACGTGCTCCAGGAACAAGCCCTC 1574
QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
DB 1575 CTGAGAGCTCAAGGCTGGCTTA-----GAATATGCGCTCCCGGGGCACATCAAC 1625
QY 497 LeuIleValIleGlyTyrglyArgProLeuGluHisProHisProGlyIleLeuGlnLys 516
DB 1626 GTCAATTAATGCAAGTGAAGCTGTGAAGCAATGAAG-----GTGAAGAGCTGAAG 1679
QY 517 GluSer-----ValSerPheValSerTrpLysGlyGlyLysSerLysHisSerGly 533
DB 1680 CGGGTAAAGAGCGGTCAAGCGTCAATTAATGAAGAGAGAAATCAAGTATCCAG 1729
QY 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerLysSer 553
DB 1740 GCGAGTTCCTGAAGAGCTTCCAGGTGCTCAAGGCTCAAGGAGAGAG-----AGTCCC 1790
QY 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnAlaArg 573
DB 1791 AGGTGTCT-----AGCAATGACAAAGAGG--TCTCTCTCAATCATCTCCGAAAA 1840
QY 574 ArgSerArgLeuLysGluProProGluLeuGlnSerGluArgAlaAlaGlySer--- 592

AC AAA09048;
 XX
 DT 01-AUG-2000 (first entry)
 XX
 DE Fusion polypeptide 569, IL-1 trap coding sequence.
 XX
 KM IL-1 trap; cytokine; antagonist; CNTF; receptor; fusion protein;
 XX cytostatic; immunomodulator; osteopathic; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN MO200018932-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99MO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0113942.
 XX
 (REGG-) REGENERON PHARM INC.
 Stahl N, Yancopoulos GD;
 MPI: 2000-293165/25.
 DR P-PsDB; AA92206.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 XX or disorders encodes a fusion polypeptide capable of binding a cytokine
 XX to form a nonfunctional complex
 PS Example 6; Fig 26A-E; 152pp; English.
 XX
 CC This sequence encodes fusion polypeptide 569, which is capable of
 CC binding cytokine IL-1 to form a non-functional complex.
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 XX
 SQ Sequence 2733 BP; 823 A; 633 C; 624 G; 653 T; 0 other;
 Alignment Scores:
 Pred. No.: 5,06e-157 Length: 2733
 Score: 1930.00 Matches: 357
 Percent Similarity: 99.72% Conservative: 0
 Best Local Similarity: 99.72% Mismatches: 1
 Query Match: 52.60% Indels: 0
 DB: 21 Gaps: 0

QY 1 MetThrLeuLeuTrpCysValValSerLeuTrpPheTrpGlyIleLeuGlnSerAspAla 20
 |||
 DB 1 ATGGTGCCTTCTGTGGTGTGTAGTGTCTTACTTTATGCAATCTCCAAAGTATGCC 60
 QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
 DB 61 TCAGAACGCTGAGTGAATCTGGGGACTAGACACATGAGGCAAAATCCAGTGTTCAGAT 120
 QY 41 GluProAlaArgIleLeuGlyCysProLeuPheGlnIleSphenLeuLysPheAsnTrpSerThr 60
 DB 121 GAGCCAGCTCGCATCAAGTCCACTCTTGAACACTTCTGAAATTCACATCAAGCACAA 180
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTrpTrpArgGlnAspArgAspLeuGlu 80
 DB 181 GCCCATTCAGCTGGCTTACTGTGATCTGGTATGTAAGTACAGGACGACCGGACCTTGAG 240
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
 DB 241 GAGCCAACTTAATCTCCGCTCCCGAGAACCGCATTAAGTAAAGAGAAAGATGCTGTGG 300
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpTrpCysMetLeuArgAsnThrThr 120
 DB 301 TTCGGCCCACTCTCTCATATGACATGCGCAACTATACCTGATCTTAAGGAACACTACA 360
 QY 121 TyrCysSerLysValAlaPheProLeuGluValAlaGlnLysAspSerCysPheAsnSer 140
 DB 361 TATGTCAGCAAAAGTTCATTTCTTGAGAGTTGTTCAAAAGACAGCTGTTCATATTC 420
 QY 141 PrometLysLeuProValHisLysLeuTrpIleGluTrpGlyIleGlnArgIleThrCys 160
 DB 421 CCATGAAGAACTCCAGTGCATTAATCTATATAGATATGAGATTCAGAGATCACTTGT 480
 QY 161 ProAsnValAspGlyTrpPheProSerSerValLysProThrIleThrTrpTrpMetGly 180
 DB 481 CCAAAATGATAGATGATATTTCTTCCAGTGCACCAACGATCATCTTGATATGGGC 540
 QY 181 CysTrpLysIleGlnAspPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 DB 541 TGTATTAAATACAGAAATTTTATATGTAATACCCGAAAGTATTAATCTGATTTCTTC 600
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTrpTrpCysValValThrTrpProGluAsnGly 220
 DB 601 ATTCGCTTAATTTCAAAATATGAGAAATTAACATGTGTGTATCAATCCAGAAATGCA 660
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 DB 661 CGTAGCTTTCATCTCACAGAGACTGTGACTGTAAAGTAGTAGGCTTCCAAAATAATGCA 720
 QY 241 ValProProValIleHisSerProAsnAspHisValValIleTrpGluLysGluProGluGlu 260
 DB 721 GAGCCCCCTGTATATCATCTACCTATATATCATGTGTGTATGAGAAAGAACACAGAGAG 780
 QY 261 GluLeuLeuIleProCysThrValTrpPheSerPheLeuMetAspSerArgAsnGluVal 280
 DB 781 GAGCTACTCATTCCTGTAGCGGTATTTAGTTTTCGATGATATTCGCAATAGAGTT 840
 QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 DB 841 TGGTGCACCATTTAGGAAAAAACCTGATGACATCATTTGATGATGCCATTTAACGAA 900
 QY 301 SerIleSerHisSerArgThrGluAspGluThrArgTrpGlnIleLeuSerIleLysLys 320
 DB 901 AGTATTAAGTCATAGTAAACAGAAATGAAATCAACAACTCATTTTATGATCAAGAA 960
 QY 321 ValIleThrSerGluAspLeuLysArgSerTrpValCysHisAlaArgSerAlaLysGlyGlu 340
 DB 961 GTTACTCTGAGAGATCTCAAGGCGAGTATGTCTGTCAATGCTAGAAAGGCCAAAGCGAA 1020
 QY 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTrpThrVal 358
 DB 1021 GTTGCCAAAGAGCCCAAGGTGAAGCAAAAGTCCAGCTCCCAAGATACACAGTGTG 1074


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Db 1125 GATGCCATCTCTCTTACACAAAGGAGCCAGATCTTACCTGTGACATCTCTGAA 1184
Qy 417 GUGUGUGUUPheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLys 436
Db 1185 GAAGAGCAGTTGCTCTTGAAGTACTCCAGAGTCTCTGAGAAACATATGATATAA 1244
Qy 437 LeuGlyPheAspArgSerLeuProGlyGlyAsnThrValGluValPheAsp 456
Db 1245 CTCTTCATCCGAGAAAGAGCCTGATTCAGAGTGAACATCAATGGAAGATCTCACAGA 1304
Qy 457 PheLeuArgSerArgMetLeuValLeuSerProAspTyrValThrGlyLys 476
Db 1305 TATGTTGAACAGAGAGAGACTTATATGCTCTAATCCAGACATATATCTCAGACG 1364
Qy 477 SerLeuMetLeuGluPheGlyValMetCysGlnAsnSerLeuAlaThr 495
Db 1365 GGATGGAGTATTTTTCGAACTGGAAGCAGACTCATTAACATGCTAGTCACTGGA 1418
Qy 496 LysLeuLeuValGluTyrArgProLeuGluHisProHisProGly 511
Db 1419 GAATCAAAAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1466
Qy 512 IleLeuGluLeuGlyGluSerValSerPheValSerTyr 524
Db 1467 AATTCGAGAGAGTGAATCATCTAAAGCCTAGATCAAACTTCTGCTCTGATCAAGTG 1526
Qy 525 LysGlyGluLeuSerLeuHisSerGlySerLeuPheTyrLysAlaLeuArgLeuAlaLeu 544
Db 1527 AAGGATCCAAAGAGAGCAAAATTAATCTAAGTTTGAGAGCACTTATATGATAAG 1586
Qy 545 ProLeuArg 547
Db 1587 CCCATCAAGAAAGAAAGAAATGCTACTCGGTCGATGTTCTGAGCTCCGAGAACAGGA 1646
Qy 548 SerLeuSerAlaSerSerGlyTyrPheAsnGluSer 558
Db 1647 CTTTTGAGAGACTCCAGCTTATACCTCTATTTGCATACACAGTACTTACAGCACTTG 1706
Qy 559 CysSerSerGlnSerAspLeuSerLeuAspHisValGlnArgArgSerArgLeuLys 578
Db 1707 GTGTCATCTCAGCTGATCTC 1727
Qy 579 GluProGluLeuGlnSerSer 586
Db 1728 CTTGAATTCACCCCTTCAAGTCAATGCAATGAGCAGCTGTTGAGAGGTTAT 1781
Qy 587 GluArgAlaAlaGlySerProAlaProGlyMetSerLysHisArgGly 604
Db 1782 AATCATGATGATACAGCCAGCAGCTTGCAGATACCTTCTTACGACACACAT 1835
Qy 605 LysSerSerAlaThrCysArgCysValThrTyrCysGluGlyGluAsnHisLeuArg 624
Db 1836 ACTTATTTGTAACCTGCTGAGCTGAGCTACTCAAGGAGCAGTACCCCTTAT 1886
Qy 625 Asn 632
Db 1887 AACACCTGAAGATACCAAGAAATTTTAC 1916

```

```

OS Homo sapiens.
XX W0919480-A2.
XX 22-APR-1999.
XX 14-OCT-1998; 98WO-US20939.
XX 10-AUG-1998; 98US-0095987.
XX 15-OCT-1997; 97US-0951829.
XX 17-NOV-1997; 97US-0971635.
XX 12-MAR-1998; 98US-0078008.
XX 18-MAR-1998; 98US-0040714.
XX 15-APR-1998; 98US-0081883.
XX (SCHE ) SCHERING CORP.
XX Bazan JF, Debets JEMA, Kastelein RA, Sana TR, Timans JC;
XX WPI; 1999-326545/27.
XX Interleukin-1 receptor-like polypeptides RD8, 9 and 10
XX Claim 28; Page 88-91; 150pp; English.
XX This sequence encodes a interleukin-1 (IL-1) receptor-like polypeptide,
XX designated IL-1 receptor DNAx designation 8 (IL-1RD8), of the
XX invention. The IL-1RD8, IL-1RD9, and IL-1RD10 proteins, their fragments
XX and mutants, also related antibodies, other binding agents and
XX (anti)agonists are used to treat conditions associated with abnormal
XX expression of the polypeptide or abnormal expression of, or response to,
XX their ligands, e.g. immunological, inflammatory or morphological
XX disorders. They may also be used to screen for binding agents (potential
XX drugs), diagnostic reagents (to detect the proteins or their ligands) and
XX to isolate related sequences. Antibodies may also be used to raise
XX anti-idiotypic antibodies, as carriers for toxins, radionuclides or other
XX therapeutic agents, and for affinity purification.
XX
XX Sequence 1737 BP; 566 A; 330 C; 397 G; 444 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 2,17e-59 Length: 1737
XX Score: 600.00 Matches: 207
XX Percent Similarity: 51.44% Conservative: 96
XX Best Local Similarity: 35.14% Mismatches: 208
XX Query Match: 21.80% Indels: 78
XX DB: 20 Gaps: 24
XX
XX US-10-061-727-2 (1-687) x AAX58247 (1-1737)
Qy 1 MethrLeuLeuTyrCysValAlaSerLeuTyrPheTyrGlyIleLeuGlnSerAsp 19
Db 7 CTCACACTATTA-----GTGTCAACAATGCTCACTGATCTTATACCTTCTGATTT 60
Qy 20 ---AlaSerGluArgCysAspSerTyrGlyLeuAspHisMetAlaGlnIleValPhe 38
Db 61 CTTTCAAGTGAAGTGTGATTTGATGCTGATGAT---CTCAAGACATACATGAGCTTTG 117
Qy 39 GluAspGluProAlaArgIleCysProLeuPheGluHisPheLeuLysPheAsnTyr 58
Db 118 GCAGTGAACACAGTCCAGAGTGAATGTCCTTTTCTACAGTATATTCATCCACATAT 177
Qy 59 SerThrAlaHisSerAlaGlyLeuThrLeuLeuTyrTyrThrArgGlnAspArgAsp 78
Db 178 AGCAGGCGCCAGACAGCAGCTGAGCTCAGCTTATGTTGTAAC-----AAAAACAAAGTGAT 231
Qy 79 LeuGluGluProIleAsnPheArgLeuProGluLysAsnArgIleSerLeuGluLysAspVal 98
Db 232 TTGAAGAGCCCATCATCTTT-----TCAGAGTTCAGAGTGAAGCAAGAGAGATTTCA 285
Qy 99 LeuTyrPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuAsn 118
Db 286 ATATGGTTTCACTCAGCTGAGGCAAGACAGTGAATTTCTACCTTGTGTTTAAGGAC 345

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QY 119 ThrThrTyrCysSerLysValAlaPheProLeuGluValAlaGlnLysAspSer----- 136
DB 346 TCAACATATTCGATGAGAGTGTCCATGTCCTGACCTGTCGACGAGAAATGATCAGGCTCG 405
QY 137 CysPheAsnSerPheMetLysLeuProValHisLysLeuTyrTlleGluTyrGly----- 154
DB 406 TGTCTACACAGCAGAGATCCGCG-----TATTATGAAAATCTGGAAGTC 447
QY 155 -----IleGlnArgLleThrCysProAsnValAspGlyTyrPheProSerSerValLys 172
DB 448 ACTAAAAGAAAGAGAGATCTCTGTCCAGACATGATGACTTTAAAAAGTCCGATCAGAG 507
QY 173 ProThrLleThrTyrPheTyrMetGlyCysTyrLysIleGlnAsnPheAsnValIlePro 192
DB 508 CTGATGTTGTGTGTGTTAAGAAATTCAGACCCAAATGTCGAGAACTAATTAATACAG 567
QY 193 GlnGlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyLysAsnTyrThrCys 212
DB 568 AAGAGAAATGCTCTCTGATCCAGAAAGTTCAAGAAAGATGAGAAATTCACATGCT 627
QY 213 ValValaThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLys 232
DB 628 GAACCTTAAATAT-----GAGGAAAACTT-----GTAAAGACAACTGAATTTGAAA 675
QY 233 ValValaGlySerProLysAsnAlaValPro-----ProValIleHisSerProAsnAspHis 251
DB 676 GTTACAGCTTTACTCAGACAGCAAGCTCCCAAGCATTGTTCCCATGAGATTCAGCCA 735
QY 252 ValValaTyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSer 271
DB 736 AGTGTTATGATGATGTCAGAGCTGGTAAAGCTCTGACATCCCTCGAAGACATCTTCGGA 795
QY 272 PheLeuMetAspSerSerArgAsnGluValTyrTyrThrLleAspGlyLysLysProAspAsp 291
DB 796 TTCAGTGAAGAGCTGGCGCAATGATCTACTGCG--ATGAAAGAGGAAAG----- 843
QY 292 IleThrLleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThr 311
DB 844 -----TTTATTGAAAGACTGGCAGCTCAGCTTGA--GAGGTGAAATA 885
QY 312 Arg-----ThrGlnIleLeuSerIleLysLys 330
DB 886 AGGCTTCTCAAGAGATCTTGGAGAAAAGATTGAATTGACATCTTGACTCA 945
QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
DB 946 GTTGTGAAGCTGACCTG--GCGAATTATACCTGCGCATGTTGAAAACCGAAATGACGG 1002
QY 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
DB 1003 -----AAACATGCCAGTGTGCTGCGTAAAAAGATTTAATCTATTAATAATTGACCTT 1056
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380
DB 1057 GCAGGGGGCTGGGAGAGAACTTCTCTCTCTGTAAGTGGTGGTGCATTTACAATATGC 1116
QY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
DB 1117 TACAACATTTGAATGATGCTCTTCTACAGCAGCATTTGAGCTGATGAATAATGAT 1176
QY 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArg----- 413
DB 1177 GACAAACAGAAATGATGCTTCTCTTACACAAAGTGACCAAGATACCTTTAGAC 1236
QY 414 -----AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsn 431
DB 1237 TGTGACATCTCTGAAGAGAGCAGCTTGTCTTGAAGTACGCAAGATGCTCGTGA AAAA 1296
QY 432 GluPheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThr--- 450
DB 1297 CACTATGATATTAATCTTCTATCCAGAAAAGACCTGATTCAGAGTGGAAAGCATAC 1356

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QY 451 ValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerPro 470
DB 1357 ATGGAAGATCTTCAGAAATATGTTTGAACAAAGACAGAACTTATTAATGCTTAACCTCA 1416
QY 471 AspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
DB 1417 GACTATATTTCTGACAGCGGAGTGGAGTAT-----TTGAACTGGAAGACAGACTCCAT 1470
QY 491 AsnSerIleAlaThr-----LysLeuIleValValGluTyrArgProLeuGluHis 507
DB 1471 AACATGCTAGTCAAGTGGAGAAATCAAGATGATTTGATGAGTGAACAGATTAAAA--- 1527
QY 508 ProHisProGly-----IleLeuGlnLeuLysGluSerVal----- 519
DB 1528 -----GGGAAAGTGAATTGCCAGAGAGTGGATCACTAAAGCTGACATCAAACTT 1578
QY 520 ---SerPheValSerThrLysGlyLysLysSerLysHisSerGlySerLysPheTrpLys 538
DB 1579 CTGTCCCTGATCAAGTGGAGGATCCAAAGCAGCAAAATTAATTTAAGTTTGGAAAG 1638
QY 539 AlaLeuArgLeuAlaLeuProLeuArg 547
DB 1639 CACTTATGATGAATGCCCATCAAG 1665
RESULT 12
AAD27169
ID AAD27169 standard; DNA; 1737 BP.
XX
AC AAD27169;
XX
DT 09-APR-2002 (first entry)
DE Human interleukin-1 receptor DNA designation 8 (IL-1RD8) DNA #1.
XX
DE Human; morphogenesis; immune system; interleukin-1 DNA designation 8;
XX IL-1RD8 protein; therapy; immunological disorder; ds.
XX
OS Homo sapiens.
XX
FH
FT 1.1737
FT CDS
FT /tag= a
FT /product= "Human IL-1RD8 protein"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN US6326472-B1.
XX
PD 04-DEC-2001.
XX
PF 14-OCT-1998; 98US-0173151.
XX
XX 15-OCT-1997; 97US-062066P.
XX 17-NOV-1997; 97US-065776P.
XX 12-MAR-1998; 98US-078008P.
XX 18-MAR-1998; 98US-078416P.
XX 15-APR-1998; 98US-081883P.
XX 10-AUG-1998; 98US-095987P.
XX
XX (SCHER) SCHERING CORP.
XX
XX Timans JC, Debets JEMA, Sana TR, Bazan JF, Kastelein RA;
XX WPI, 2002-121110/16.
XX P-PDB; AAE16566.
XX
XX Antibody fragments which specifically bind to primate interleukin 1
XX receptor-like molecules are useful to treat conditions associated with
XX abnormal expression of the receptor or its ligand, particularly
XX immunological disorders
XX
XX Disclosure; Column 7-10; 102pp; English.
XX

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CC The present invention relates to compositions and methods for affecting
 CC mammalian physiology such as morphogenesis of immune system function.
 CC The invention particularly relates to nucleic acids, proteins and
 CC antibodies which regulate development and/or the immune system. The
 CC invention also relates to antibody fragments which specifically bind
 CC to antigenic fragments of a primate interleukin (IL)-1 receptor like
 CC molecules such as IL-1 receptor DNAx designation (IL-1RD). The antibody
 CC fragments of the invention are useful to treat conditions exhibiting
 CC abnormal expression of the receptors or their ligands which typically
 CC will be immunological disorders. The present sequence is a DNA encoding
 CC human IL-1RD protein.

XX Sequence 1737 BP, 566 A, 330 C, 397 G, 444 T, 0 other;

Alignment Scores:

Pred. No.:	2.17e-59	Length:	1737
Score:	800.00	Matches:	207
Percent Similarity:	51.44%	Conservative:	96
Best Local Similarity:	35.14%	Mismatches:	208
Query Match:	21.80%	Indels:	78
DB:	24	Gaps:	24

...10-061-727-2 (1-687) x AAD27169 (1-1737)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTrpPheTrpGlyIleLeuGlnSerAps--- 19
 Db 7 CTCACACATATTA-----GTGTCAACATATGCTCAGTATCTTATACCTCTTCTGATTTT 60
 Qy 20 ---AlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgIleGlnValPhe 38
 Db 61 CTTTCAGTGGATGGCTGATTCAGTGCATGAGAT---CTCAACACATATACGCTTGG 117
 Qy 39 GlnAspGluProAlaArgIleLeuCysProLeuPheGlnHisPheLeuLysPheAsnTrp 58
 Db 118 GCAAGGTGACAGCTCCGAGTGAATGTCCTTTTCTACAGTTATATTCGATCCAACTAT 177
 Qy 59 SerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTrpTrpThrArgGlnAspArgAsp 78
 Db 178 AGCAGCGCCGACAGACACAGCTGCTCAGCTTATGCTGTC-----AAAAACAAGGTGAT 231
 Qy 79 LeuGlnGluProIleAsnPheArgLeuProGlnAsnArgIleSerIleGlnLysAspVal 98
 Db 232 TTGGAAGGCCCATCATCTTT-----TCAGAGTCAGAGATGAGCAAGAGAGATTC 285
 Qy 99 LeuThrPheArgProThrLeuLeuAsnAspArgIleGlnValTrpTrpCysMetLeuArgAsn 118
 Db 286 ATATAGGTTCTCTAGCTGAGGCAACAGACAGTGAATTCCTACCTGTTTAAAGAAC 345
 Qy 119 ThrThrTrpCysSerLysValAlaPheProLeuGlnValValGlnLysAspSer----- 136
 Db 346 TCACATATATGCAATGAGTGTCTGATGCTTGTGACGTTCGACAGAGATGAATGAGGCTTG 405
 Qy 137 CysPheAsnSerProMetLysLeuProValHisLysLeuTrpIleGluTrpGly----- 154
 Db 406 TGCTACAAACAGCAGATCCGC-----TATTAGAAAATATCGAAGTC 447
 Qy 155 -----IleGlnArgIleThrCysProAsnValAspGlyTrpPheProSerSerValLys 172
 Db 448 ACTTAAAGAAAGAGATCTCTCTGTCAAGACATGATGATCTTAAAGATCCGATCAGAG 507
 Qy 173 ProThrIleThrTrpTrpMetGlyCysTrpLysIleGlnAsnPheAsnValIlePro 192
 Db 508 CCGTATGTGTGTGTATAGAGATGCAAGCAAAATGTGAGAGATATATATATACAG 567
 Qy 193 GlnGlyMetLeuLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTrpThrCys 212
 Db 568 AAAGGAATGCTCTTCTGATCCAAAGATTCAGAGAGAGATGAGAAATTAACATGT 627
 Qy 213 ValValThrTrpProGlnAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLys 232
 Db 628 GAACCTTAATAT-----GAAGGAAACTT-----GTAGAGCAACAATGAAATTTAAA 675
 Qy 233 ValValGlySerProLysAsnAlaValPro---ProValIleHisSerProAsnAspHis 251

Db 676 GTTACAGCTTATCTACAGACAGACAGCTTCCAGGCAATGTTCCCAAGAGAAATACGCA 735
 Qy 252 ValValTrpGluGluProGluGluLeuLeuIleProCysThrValTrpPheSer 271
 Db 726 AGTGTATATAGATGTCAGAGCTGGTAAAGCTCTGAACATCCCTTCAAGACATTTCTGGA 795
 Qy 272 PheLeuMetAspSerArgAsnGluValTrpThrIleAspGlyLysProAspAsp 291
 Db 796 TTCAGTGAAGAGCTGGGCCAATGATCTACCTG---ATGAAGGAGAAAG----- 843
 Qy 292 IleThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGlnAspGluThr 311
 Db 844 -----TTTATGAAAGAACTGGCAGCTCACTTAA---GAAGGTGAATA 885
 Qy 312 Arg-----ThrGlnIleLeuSerIleLys 320
 Db 886 AGGCTTCTCAAGAGCATCTTGGAGAAAGAAAGATGGAATTTGGACATCTTGTGACTCA 945
 Qy 321 ValThrSerGluAspLeuLysArgSerTrpValCysHisAlaArgSerAlaLysGlyGlu 340
 Db 946 GTTGTGAAGCTGACCTG---GCCAATTATACCTGCATGTGAAACCGAAATGACCG 1002
 Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTrpThrValGluLeu 360
 Db 1003 -----AAACATGCGCACTGTGTTGCTGCGTAAAGAAAGATTTAATCTTAAATTTGACCTT 1056
 Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTrpHisVal 380
 Db 1057 GCAGGGGCGCTGGAGAGCAATCTTCTCTCTTCTGCTGCTGGTGGTATTTCAAAATGC 1116
 Qy 381 TyrTrpLeuMetValIlePheTrpArgAlaHisPheGlyThrAspGluThrIleLeu 400
 Db 1117 TACAACATTTAATGATGCTCTTCTACAGACACACTTGGAGTGATGAATGAT 1176
 Qy 401 AspGlyLysGluTrpAspIleTrpValSerTrpAlaArg----- 413
 Db 1177 GACAACAGAAATATATGATGCTTCTCTTACCAAAAGATGACCAAGATACTTTAGAC 1236
 Qy 414 -----AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgValLeuGluAsn 431
 Db 1237 TGTGACATCTCTGAAGAGAGAGCTTGTCTTGAAGTACTGCCAATGCTCTGGAAAA 1286
 Qy 432 GluPheGlyTrpLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThr--- 450
 Db 1297 CACTATGATATTAACCTTCTCATCCAGAAAGAGACCTGATTCAGATGGAAGTCATAC 1356
 Qy 451 ValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerPro 470
 Db 1357 ATGGAGATCTCAACAGATATGTTGAACAAAGCAAGACCTTATTTTTCGGCTAACTCCA 1416
 Qy 471 AspTrpValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
 Db 1417 GACTATATTTCTAGACGGGATGAGTATTT-----TTGGAATCGAAAGACATCTCCAT 1470
 Qy 491 AsnSerIleAlaThr-----LysLeuIleValValGluTrpArgProLeuGluHis 507
 Db 1471 AACATGCTAGTCACTGAGAAATCAAGATTTTATGATGAGTACAGAAATTAATA--- 1527
 Qy 508 ProHisProGly-----IleLeuGlnLeuLysGluSerVal----- 519
 Db 1528 -----GGGAAAGTGAATTCGCAAGAGAGGATCACTAAAGGTGACATCAAACTT 1578
 Qy 520 ---SerPheValSerTrpLysGlyLysSerLysHisSerGlySerLysPheTrpLys 538
 Db 1579 CTGTCCCTATATCAAGTGAAGGATGCCAAGACAGCAATTAATTTTAAAGTTTGGAAAG 1638
 Qy 539 AlaLeuArgLeuAlaLeuProLeuArg 547
 Db 1639 CACTATGATATGAATATGCCATCAAG 1665
 RESULT 13
 AAA27919


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Oy 367 ThrValleuLeuValValIleleuIleValValTyrHisValTyrTrpLeuGluMetVal 386
Db 1099 ATACTCTTGCTGCTGTGTATGTTTGTGTGACACTTACACTTTACACATGACATGCTGTG 1158
Oy 387 LeupheTyArgAlaHisSphGlyThrAspGluThrIleleuAspGlyLysGluTyrAsp 406
Db 1159 CTCCTTCAACAGAAATCATTTTGGAGCTGAGAGCTGCAGTGAAGACAAATAAAGATTATAT 1218
Oy 407 IleTyValSerTyTyrAlaArg-----AsnAlaGluGlu 417
Db 1219 GCATACCTATATATACACAAAGTGATCCTGACAGTGAATCAAGAGACTGGGAGAGAA 1278
Oy 418 GluGluPheValIleleuThrleuArgGlyValleuGluAsnGluPheGlyTyrTyrLeu 437
Db 1279 GAACTTTTGCCCTTGAAATCTTACCTGATATGCTTGAAGAAAGCATTTATGATTAAGTTG 1338
Oy 438 CysIlePheAspArgAspSerleuProGlyLysThrValIleGluAlaValPheAspPhe 457
Db 1339 TTTATACCAAGATAGAGATTTATATCCCACTGGAACATACATTGAAGATGTGCAAGATGT 1398
Oy 458 IleGluArgSerArgArgMetIleValIleuSerProAspTyrValThrGluLysSer 477
Db 1399 GTACATCAAAAGCAAGCGGCTGATTTATGTCAATGACCCCAATTAAGTATAGAAAGGCGC 1458
Oy 478 IleSerleuGluPheLysleuGlyValMetCysGlnAsnSerIleAlaThr----- 495
Db 1459 TGGAGCATC-----TTTGACCTGGAAACCAAGACTTCAAAATATGCTTGATGAGAGAA 1512
Oy 496 ---LysleuIleValIleGluTyrArgProleuGluHisProHisProGlyIleleuGln 514
Db 1513 ATTAAAGATTTCTAATTAATGAATGACGTAAGTACGAGA-----GGAATTAATGAC 1560
Oy 515 LeuLysGlu-----SerValSerPheValSerTyrLys 525
Db 1561 TACAGAGAGGTGAGAGCCCTGAAGACACATCAAGCTCTGACGGTCAATTAATATGGAT 1620
Oy 526 GlyGluLysSerLysHisSerGlySerLysPheTyrPheLysAlaLeuAlaLeuPro 545
Db 1621 GGACCAAAATCAACAAAGTTGAATCAAGTTGGAAGCTTCAACATATGAATATGCT 1680
Oy 546 LeuArg----- 547
Db 1681 TTTAAAGAGATAGAACCATTAACATAGACAGGCTTTAATGATCAGTGAAGAGGCTT 1740
Oy 548 -----SerleuSerAlaSerSerGlyTyrPheAsnGluSerCysSerSerGlnSerAspIle 565
Db 1741 TTGGGGGAGCTGACAGACTGTCTCGGCATTTTCATGCGCGGCGACCTCCACAGCTCTA 1800
Oy 566 SerleuAspHisValGlnArg-----ArgSerArgLeuLys 578
Db 1801 GCCACTGCCATCCAGATCTCGTTTCACTTTCAACACAGCTACCATTCACAAATGCGT 1860
Oy 579 GluProGluLeuGlnSerSerGluArgAlaIleGlnSerProProAlaProGly*** 598
Db 1861 CAGAAACACTACTACCAAGAGTATGAGTACAGCACTA-----CTCTCAACGGGACCTG 1914
Oy 599 MetSerLysHisArgGlyLysSerSerAlaThrCysArgCysValThrTyrCysGlu 618
Db 1915 CCTCTTACTTCATAGGCAATACAGCATCTACTGATACATCCCTATGACATCATCAAC 1974
Oy 619 GlyGluAsnHisleuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTyrPgl 638
Db 1975 GGGGAGCGGCGCAAGCAAAATCAAGAGGAGGAGCAAGTCAAGTGAAGCCCAACAAAC 2034
Oy 638 uThrHisleuCysLysProValProGlnGlnSer 649
Db 2035 AGTGCAATCCGCGCGCTG-TTGCCAGGGAGAAC 2067

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RESULT 14
AAK51941
ID AAK51941 standard; cDNA; 3122 BP.
XX

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AC AAK51941;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 486.
DE
XX Human cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX W0200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX 20-JUN-2000; 2000US-0598075.
XX
XX 19-JUL-2000; 2000US-0620325.
XX
XX 01-SEP-2000; 2000US-0654936.
XX
XX 15-SEP-2000; 2000US-0663561.
XX
XX 20-OCT-2000; 2000US-0693325.
XX
XX 30-NOV-2000; 2000US-0728422.
XX
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Dymnac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX P-PSDB; AAM78808.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX
XX Claim 1; Page 1748-1752; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
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XX Query Match: 21.04% Indels: 96
XX DB: Gaps: 22
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Db 532 TTGATCTCTTATACGCTACTTTACTCAAGATTTGAAGGTGTGACCAAAAGAGCTCC 591

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Copyright (c) 1993 - 2003 Compen Ltd.

OW protein - nucleic search, using frame_plus.p2n model

Run on: April 30, 2003, 10:47:55 ; Search time 53 Seconds
(without alignments)
3975.225 Million cell updates/sec

Title: US-10-061-727-2
Sequence: 1 MTLLMCVSLYFYGLQSDA.....SALALHFTDLSNNDFYIL 687

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=ini -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10061727@cgn2_1.1.32@runat.23042003.083117.7926 -NCPUR=6 -ICPU=3
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-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2586	70.5	1740	4	US-08-991-944-1 Sequence 1, Appli
2	2327.5	63.4	3355	4	US-08-991-944-3 Sequence 3, Appli
3	825	22.5	2061	4	US-09-173-151A-3 Sequence 3, Appli
4	800	21.8	1737	4	US-09-173-151A-1 Sequence 1, Appli
5	767	20.9	2537	4	US-09-173-151A-34 Sequence 34, Appli
6	528.5	14.4	1620	3	US-08-996-338-7 Sequence 7, Appli
7	528	14.4	1626	1	US-08-604-333-1 Sequence 1, Appli
8	528	14.4	1626	3	US-09-110-618-1 Sequence 1, Appli
9	528	14.4	1626	4	US-09-578-178-1 Sequence 1, Appli
10	520	14.2	1563	4	US-08-996-338-1 Sequence 1, Appli
11	495	13.5	2314	4	US-09-173-151A-9 Sequence 9, Appli
12	488.5	13.3	2356	1	US-07-821-716-3 Sequence 3, Appli

13	484.5	13.2	1782	2	US-08-381-603-3 Sequence 3, Appli
14	484.5	13.2	1782	3	US-08-924-376-3 Sequence 3, Appli
15	484.5	13.2	1782	4	US-08-685-212-3 Sequence 3, Appli
16	484.5	13.2	1782	4	US-08-466-932A-3 Sequence 3, Appli
17	484.5	13.2	1782	5	PCT-US94-02414-3 Sequence 3, Appli
18	484.5	13.2	1782	5	PCT-US96-08889-3 Sequence 3, Appli
19	482	13.1	4989	4	US-09-560-639-3 Sequence 3, Appli
20	479.5	13.1	2830	1	US-08-604-333-3 Sequence 3, Appli
21	479.5	13.1	2830	3	US-09-110-618-3 Sequence 3, Appli
22	479.5	13.1	2830	4	US-09-578-178-3 Sequence 3, Appli
23	478	13.0	1557	3	US-08-996-338-2 Sequence 2, Appli
24	478	13.0	1704	4	US-09-032-337-38 Sequence 38, Appli
25	463.5	12.6	2058	4	US-09-560-639-4 Sequence 4, Appli
26	459.5	12.5	1965	4	US-09-227-717-1 Sequence 4, Appli
27	457	12.5	2044	4	US-09-227-717-3 Sequence 3, Appli
28	446.5	12.2	2259	4	US-09-173-151A-15 Sequence 15, Appli
29	445.5	12.1	1833	4	US-09-173-151A-13 Sequence 13, Appli
30	436	11.9	1404	4	US-09-173-151A-7 Sequence 7, Appli
31	424.5	11.6	1770	2	US-08-381-603-1 Sequence 1, Appli
32	424.5	11.6	1770	3	US-08-924-376-1 Sequence 1, Appli
33	424.5	11.6	1770	4	US-08-685-212-1 Sequence 1, Appli
34	424.5	11.6	1770	4	US-08-466-932A-1 Sequence 1, Appli
35	424.5	11.6	1770	5	PCT-US94-02414-1 Sequence 1, Appli
36	424.5	11.6	1770	5	PCT-US96-08889-1 Sequence 1, Appli
37	424.5	11.6	3011	1	US-07-821-716-1 Sequence 1, Appli
38	418.5	11.4	1991	4	US-09-173-151A-19 Sequence 19, Appli
39	314	8.6	1340	4	US-09-647-826-2 Sequence 2, Appli
40	314	8.6	1366	1	US-08-091-519-12 Sequence 12, Appli
41	314	8.6	1366	1	US-08-442-043A-12 Sequence 12, Appli
42	314	8.6	1366	5	PCT-US91-03478-12 Sequence 12, Appli
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44	252	6.9	1357	1	US-08-442-043A-1 Sequence 1, Appli
45	252	6.9	1357	5	PCT-US91-03478-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-991-944-1
Sequence 1, Application US/08991944
Patent No. 6280955
GENERAL INFORMATION:
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
TITLE OF INVENTION: Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,944
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid

CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/991,944
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-014
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEO ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3355 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 135..1844
 US-08-991-944-3
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 Pred. No.: 4,14e-231 Length: 3355
 Score: 2327.50 Matches: 443
 Percent Similarity: 83.36% Conservative: 73
 Best Local Similarity: 71.57% Mismatches: 76
 Query Match: 63.44% Indels: 28
 DB: Gaps: 8
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 DB 21 SerGluArgCysAspSerTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
 DB 195 TCGAGCGCTGTGATGATCGGGAGCTAGATACCATGCGACAATCCAGTGTGAAGAT 254
 QY 41 GluProAlaArgIleLeuGlyCysProLeuPheGlnIlePheLeuLysPheAsnTyRSerThr 60
 DB 255 GAGCGCGCTCGATCAAGTGGCCCTCTTGAACCTCTCGAAGTACCACTACACACT 314
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTyRTrpThrArgGlnAspArgAspLeuGln 80
 DB 315 GCCCATTCCTGTGGCTTACCTGATCTGTACTGACGACGACGACGACGACGACGAC 374
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerIleGlnLysAspValLeuTrp 100
 DB 375 GAGCCATTAACTTCGCGCTCCGAGAAATCGCATCAGTAAGAGAAAGATGTGCTCG 434
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyRTrpCysMetLeuArgAsnThrThr 120
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 QY 121 TyrCysSerIleValAlaPheProLeuGlnValAlaGlnLysAspSerCysPheAsnSer 140
 DB 495 TACTGACGAAAGTTCATTTCCTCGAAGTGTTCAGAAAGACAGCTGTTCATTCT 554
 QY 141 PrometLysLeuProValHisIleLysLeuTyRleGluTyRGlYlleGlnArgIleThrCys 160
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QY 161 ProAsnValAspGlyTyRheProSerSerValLysProThrIleThrTrpIleMetGly 180
 DB 615 CCAATGTATGACGAGATCTTCTTCAGTGTCAACCATCGTCATCTGTATTAAGGT 674
 QY 181 CysTyRLeuIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 DB 675 TGTACTGAAATAGTGCATCTTATATGTATACCCGAGGGGATGAACTTGAGCTTTTTC 734
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyRThrCysValValThrTyRProGluAsnGly 220
 DB 735 ATCCCTGTGTTCAATACGAAATATACAAATGTGTGTATCAATCTTAATAACGGA 794
 QY 221 ArgThrPheHisLeuThrIleArgThrLeuThrValLysValAlaGlySerProLysAsnAla 240
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 QY 241 ValProProValIleHisSerProAsnAspHisValValTyRGlulysGluProGlyGlu 260
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 QY 261 GluLeuLeuIleProCysThrValTyRheSerPheLeuMetAspSerArgAsnGluVal 280
 DB 915 GAACGTGTATTCCTCGCAAAAGCTATTTCACTTATATGACCTCCCAATAGAGTC 974
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 QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
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 QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyRThrValGluLeu 360
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 QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyRHisVal 380
 DB 1215 GCTGTGTTTGGAGCCAGCGCTTCTGTAGTGTCTCATGTTGTTGTTTACCATGTT 1274
 QY 381 TyrTrpLeuGluMetValLeuPheTyRArgAlaHisPheGlyThrAspGluThrIleLeu 400
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 DB 1335 GATGAAAGAGATGATATTTATGTTCTATGACGAAATGTGAAAGAGAGAAATTT 1394
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 QY 481 LeuGluPheLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
 DB 1575 CTGAGACTCAAGCTGTGCTTA-----GAAATATAGCTCTCCGGGGCAACATCAAC 1625
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 DB 1626 GTCATTTTATGTCAGTACAAAGCTGTGAAGACATGAAG-----GTGAAGAGCTGAAG 1679

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 Qy 253 ValTYRGLuLysGLuProGlyLysLysLeuLeuLeuProCysThrValTYRPheserPhe 272
 Db 754 GTTATAGATGTCAGCTGAGTAAAGCTCTGAACATCCCTGCAAGACATTTCTTGATTC 813
 Qy 273 LeuMetAspSerArgAsnGluValTYRTPRThrIleAspGlyLysLysProAspPile 292
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 Qy 293 ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArg 312
 Db 859 -----TTTATGAAGAACTGGCAGGATCATTAGA---GAAGCTGAATAATAG 903
 Qy 313 -----ThrGluIleuSerIleLysVal 321
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 Qy 332 ThrSerGluAspLeuLysArgSerTYRValCysHisAlaArgSerAlaLysGlyGluVal 341
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 Qy 414 ---AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValIleGluAsnGlu 432
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 Qy 521 PheValSerTrpLysGlyLysLysSerLysHisSerGlySerLysPheTrpLysAlaLeu 540
 Db 1597 CTGATCAAGTCGAGAGGATCCAAAGCAGCAATTAATTTAAGTTTGAAGCACTTA 1656
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 Qy 548 -----SerLeuSerAlaSerSergly 554
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 Qy 575 SerArgLeuLysGluProGluLeuGlnSerSer----- 586
 Db 1810 -----CCTGAATTCACCCCTTCAGATTCATCAATCAATCAGGACTGT 1851
 Qy 587 -----GluArgAlaIleGlySerProAlaProGly**MetSer 600
 Db 1852 TGCAGAGGTTATAACATGATGATACAGCAGACCTTGCACTTCTTCTTGAAGCAAC 1911
 Qy 601 LysHisArgGlyLysSerSerAlaThrCysArgCysValThrTYRCysGluGlu 620
 Db 1912 CACCAT-----ACTATTTGTAACCTGCGCTGACCGCTACTCAACGACAG 1956
 Qy 621 AsnHisLeuArgAsn-----LysSerArgAlaGluIleHis 632
 Db 1957 CTACCCCTTAATTAACACCCCTGAAGATACCCAGAAATTTAC 1998

RESULT 4
 US-09-173-151A-1
 ; Sequence 1, Application US/09173151A
 ; Patent No. 6326472
 ; GENERAL INFORMATION:
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Debets, Johannes Eduard Maria
 ; APPLICANT: Antonius
 ; APPLICANT: Sana, Theodore R.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kastelein, Robert A.
 ; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: DNX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/173,151A
 ; FILING DATE: 14-OCT-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/065,776
 ; FILING DATE: 17-NOV-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/078,008
 ; FILING DATE: 12-MAR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/081,883
 ; FILING DATE: 15-APR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/095,987
 ; FILING DATE: 10-AUG-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/078,416
 ; FILING DATE: 18-MAR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/062,066
 ; FILING DATE: 15-OCT-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0767X
 ; TELECOMMUNICATION INFORMATION:

Db 1297 CACTATGAGATTAACCTTTCATCCCAAGAGACCTGATTCACAGTGAAGTGCATAC 1356
Qy 451 ValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValIleuSerPro 470
Db 1357 ATGGAAGATCTCAACAGATATGTTGACAGAGAGACTTATATACGCTCACTCCA 1416
Qy 471 AspTyrValThrGluYserIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
Db 1417 GACTATATCTTCAGACGGGATGAGTAT-----TTCAACTGGAAGACAGCTCCAT 1470
Qy 491 ArgSerIleAlaThr-----LysLeuIleValValGluTyrArgProLeuGluHis 507
Db 1471 AACATGCTACTGACGAGAAATCAAGATTTTGTATGATGCTACAGAAATTAATAA--- 1527
Qy 508 ProHisProGly-----IleLeuGlnIleuYsgIuSerVal----- 519
Db 1528 -----GGGAAGTGAATTGCCAGGAAGTGAATCACTAAAGCCTACATCAAACTT 1578
Qy 520 ---SerPheValSerTyrIleGlyGluYserLysHisSerGlySerLysPheTyrPlys 538
Db 1579 CTCTCCCTGATCAAGTGAAGGATTCAGAAAGCAAGCAATTAATTCTAAGTTTGGAG 1638
Qy 539 AlaLeuArgLeuAlaLeuProLeuArg 547
Db 1639 CACTAGTATATGAATGATGCCATCAAG 1665

RESULT 5

US-09-173-151A-34
Sequence 34, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066

FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2004
US-09-173-151A-34
Alignment Scores:
Pred. No.: 2,8e-69 Length: 2537
Score: 767.00 Matches: 210
Percent Similarity: 47.13% Conservative: 119
Best Local Similarity: 30.09% Mismatches: 274
Query Match: 20.90% Indels: 96
DB: 4 Gaps: 22
US-10-061-727-2 (1-687) x US-09-173-151A-34 (1-2537)
Qy 24 CysAspAspTyrGlyLeuAspPheThrMetArgGlnIleGlnValPheGluAspGluProAla 43
Db 7 TGCACGATGCTGCTATCATCAT---ATCAAGAAATATCAAGTTTGGTGGAGAGCTGTT 63
Qy 44 ArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHisSer 63
Db 64 CCAATCAAAATGTCACCTCTTATATGTTATATACAGAAATTAATTAATTAATTAATTAAT 123
Qy 64 AlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGluProIle 83
Db 124 GCTGACCTAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 183
Qy 84 AsnPheArgLeuProGluAsnArgIleSerLysGlyLysAspValLeuTyrPheArgPro 103
Db 184 GCCTTT-----GACGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 237
Qy 104 ThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSer 123
Db 238 ACATTGCTACAGAGAGAGTGTCTTACGCGCTGTGTATGATGATGATGATGATGATGAT 297
Qy 124 LysValAlaPheProLeuGluValValGlnLysAspSer-----CysPheAsnSerPro 141
Db 298 AAAGTATCATCTCACTGACAGTGGGTGAATAATGACACAGCTGCTATTAATTCGAAG 357
Qy 142 MetLysLeuProValHisIleLysLeuTyrIleGlyTyrGly-----IleGlnArg 157
Db 358 ATGAG-----TATTTGAAAAGCTGAACCTTAAGCAAGCAAGCAAGCAAGCAAGCA 399
Qy 158 IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyr 177
Db 400 ATTATATGCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 459
Qy 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeu 197
Db 460 TACAAGATGAGAGAGCAAAACATGAGGCGCAATGATGATGATGATGATGATGATGATGAT 519
Qy 198 SerPheLeuIleAlaLeuIleSerAsnGlnLysAsnTyrThrCysValValThrTyrPro 217
Db 520 CTTATTAAGAGAGTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
Qy 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValValValGlySerPro 237
Db 577 ---GGAGGCTTTGTTGTGTGAGAGAACTACTGATTAATTAATTAATTAATTAATTAAT 624

QY 238 LysAsnAlaValProValIleHisSerProAsnAspHis-----ValValIleTyrGlu 255
Db 625 CTGACTGATAGACCAAGCTTTTGTATCTATGGAAGTAACATGACATTCAGAG 684
QY 256 LysGluProGlyGluGluLeuIleProCysThrValTyrPheSerPheLeuMetAsp 275
Db 685 ACCAGCGTGGTGAAGCTGCTGATCTAATCTGACAGAGCTTCTTGGGTACAGGAGAT 744
QY 276 SerArgAsnGluValIleTyrTrpThrIleAspGlyLysIleProAspAspIle----- 292
Db 745 GTGAGCTCTTAAATTTAATCTGATGAAAGAGAAAATTTATTAAGATCTGATGAAAT 804
QY 293 -----ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAsp 309
Db 805 CGAGTTGGGAAAGTGAATGAAAT-----CTTAAGAGCATCTTGGGAAACAG 855
QY 310 GluThrArgThrGlnIleLeuSerIleLysIleValThrSerGluAspLeuLysArgSer 329
Db 856 GAAGTTTCCATCTCATTAAT---GTGAGCTGTGGAAGAGGTAAGTCTG---GGAAT 909
QY 330 TyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaLysValLysGln 349
Db 910 TACTCTGTATGTGAAATAAGAAATGAGAGCT-----CGACACGCGCAGGCTCTCCTT 963
QY 350 LysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAlaThrValLeu 369
Db 964 CATTAACAGACAGCTAATGTATACAGGTGAGCTGTGAGGCTTGGTGTATATCTTGT 1023
QY 370 LeuValValIleLeuIleValIleValIleValIleValIleValIleValIleValIle 389
Db 1024 CTGCTGTGATGTTTGTGACCATCTACAGGTGTAACAAGATAGAAATATATCTTCTTAC 1083
QY 390 ArgAlaHisPheGlyIleThrAspGluThrIleLeuAspGlyLysIleTyrVal 409
Db 1084 AGGATCATTTTGGAGCTGGAAGAGCTCGATGAGACATTAAGATTAAGATGATCTTCTTA 1143
QY 410 SerTyrAlaArg-----AsnAlaGluGluGluGluPhe 420
Db 1144 TCATTAACCAAGAGTATCTGACCATGGAATCAAGAGCTGGGAAAGAAAGCTTTT 1203
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrIleLysCysIlePhe 440
Db 1204 GCCCTTGAATCTTACCTGATATGCTTGAAGAAAGCTTATGATATTAAGTTTATATCA 1263
QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1264 GATGAGATTTAATCCCAACTGMAATGMAATGAGTGGCAAGATGTGTAGATCAA 1323
QY 461 SerArgArgMetIleValIleLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1324 AGCAAGCGGCTGATATGTATGATGACCCCAATTAAGATTAAGAGGAGCTGAGACATC 1383
QY 481 LeuGluPheLysLeuGlyValMetCysGluAsnSerIleAlaIle-----LysLeu 497
Db 1384 -----TTTGAAGCTGAAGACCAAGACTTGAATAATGCTTGTGACAGGAATTAAGTG 1437
QY 498 IleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGluLeuLysGlu 517
Db 1438 ATTTCAATTAAGATGACAGTGAAGTGA-----GGAATTAATTAACATACAGAGAG 1485
QY 518 -----SerValSerPheValSerThrLysGluGluLys 528
Db 1486 GTGAGAGCCCTGAAGACACATCAAGCTCTGAGGCTCATTAATTAAGTACAGACCAAA 1545
QY 529 SerLysHisSerGlySerLysPheTyrLysAlaLeuArgLeuAlaLeuProLeuArg--- 547
Db 1546 TGCAACAGTGAATCAAGTCTGGAAGAGCTTACAGTATGAATATCCCTTTTAAGAGG 1605
QY 548 -----Ser 548
Db 1606 ATAGAACCATTAACATGAGCAGGCTTATGATGTCACTGAGCAAGGAGCTTTTGGGAGG 1665

QY 549 LeuSerAlaSerSerGlyTyrAsnGluSerCysSerSerGlnSerAspIleSerLeuAsp 568
Db 1666 CTGCACATGCTGTGCGCCATTTTCCATGCGCGGCGCACCTCCACAGCTACGACCTGCC 1725
QY 569 HisValGlnArgArg-----ArgSerArgLeuLysGluProPro 581
Db 1726 CATCCAGATCTCGTCTTACTCTTTCACAAACAGCTACCATTCACAAATGCGTCAAGAAC 1785
QY 582 GluLeuGlnSerSerGlnArgAlaAlaGlySerProAlaIleProGly**MetSerLys 601
Db 1786 TACTACCGAAGCTATGATGACAGTGA-----CTTCTTACCGGACAGCTGCTTACC 1839
QY 602 HisArgGlyLysSerSerAlaThrCysArgCysCysValIleThrTyrCysGluGluGlu 621
Db 1840 TCCATAGGCAATGAGATATCTTATCTTATACATCCCTATGACATCTATCAACGGGACGG 1899
QY 621 HisLeuArgAsnLysSerArgAlaGluIleHisAsnGluProGlnTrpGluThrHisIle 641
Db 1900 CCACAGACAAATGACAGCAGGAGCAGAAATCCAGATGAGGCGCCACAAACAGTGCATC 1959
QY 641 UCysLysProValProGluGlu-----SerGluThrGlnTrpIleGln 655
Db 1960 CTGCGCGCTG-TTGCCAAAGGAGACAGATATTCAGTGTGATGATGAGACAG 2010

RESULT 6
US-08-996-338-7
Sequence 7, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:

NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/604.333
 FILING DATE: 21-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2619
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEEX: 756822
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1626 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: hu2P1
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1626
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 58..1623
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 1..57
 US-08-604-333-1
 Alignment Scores:
 Pred. No.: 8,48e-45 Length: 1626
 re: 528.00 Matches: 174
 ent Similarity: 46.03% Conservative: 93
 Last Local Similarity: 30.00% Mismatches: 215
 Query Match: 14.39% Indels: 98
 Gaps: 27
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 QY 4 LeuTPCyValValSerLeuTYrPheTYrGlyIleLeuGlnSerAspAlaSerGluArg 23
 DB 28 CTTTGGGCTTATATCTGTA-----AGCACTGCAGAACTCT 63
 QY 24 CysAspAspTrpGlyLeuAspThrMetArg-----GlnIleGlnValPheGlnAspGluPro 42
 DB 64 TGT-----ACTTACGTCCTCCACATTACTGTGTTGAAGCGGAACCT 105
 QY 43 AlaArgIleLys---CysProLeuPheGlnHisPheLeuLysPheAsnTYrSerThrAla 61
 DB 106 TTTCTATCTGAAACATTC-----TCGTGTTCACTTGCA 138
 QY 62 HisSerAlaGlyLeuThrIleu---IleTPYrTYrTrpThrArgGlnAspArgAspLeuGlu 80
 DB 139 CATTGACATTGAACACACCAAAAGCTGTATCAAAAGAGTGATCAAGAACTGTG 198

QY 81 GluProIleAsnPheArgLeuProGlnAsnArgIleSerLysGluLysAspValLeuTrp 100
 DB 199 GAG---CTGAACCCAAAG---AGTTCCTCGAAGATTGCTTGTCATGATGTGTTTGAG 252
 QY 101 PheArgProThrIleLeuAsnAspThrGlyAsnTYrThrCysMetLeuArgAsnThr 120
 DB 253 TTTTGCCAGTTGAGTTGATGACAGAGATCTTACTTTTCCAAATATAATATATCT 312
 QY 121 TYrCysSerLysValAlaPheProLeuGluValValGln-----LysAspSerCysPhe 138
 DB 313 CAG-----AAATGAAATTAATGTCATCAGAAAGAAATTAACACAGCTGTTTC 360
 QY 139 Asn-----SerProMetLysLeuProValHisLysLeuTYrIleGluTYrGly 154
 DB 361 ACTGAAGACAGTAAGTAAGTAAATGTGAAAGTTAAATAATTTTTT----- 408
 QY 155 IleGlnArgIleThrCysProAsnValAspGlyTYrPheProSerSerValLysProThr 174
 DB 409 -----CAGATTAACCTGTGAAAC-----AGTTACTATCAAAACCTGCTCAACAGACA 456
 QY 175 IleThrTPYrMetGlyCysTYrLysIleGlnAsnPheAsnAsnValIleProGlu--- 193
 DB 457 ---TCATTGTATTAAGAACTGTAAAGCTACTCTGAGAACATTAATAAACCAAGATA 513
 QY 194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTYrThrCysVal 213
 DB 514 AAGAAAGACGCCGAGTTT-----GAAATACAGGGGTATTAATCTCGCGTG 558
 QY 214 ValThrTYrProGlnAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 233
 DB 559 CATTTCCTTCATCATATGAAAGAACTATTATATACCAAAACCTTCATATTAACATA 618
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 DB 619 GTGAAAGATCGAGTAATATATGTTCCGTTCTTTCGACCAAACTTAACATGTTGCA 678
 QY 254 TYrGluLysGluProGlyGlnGluLeuLeuIleProCysThrValTYrPheSerPheLeu 273
 DB 679 GTGGAATTA-----GGAATAACGTAAAGCTCAACTGC-----TCTGCTTGG 720
 QY 274 MetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThr 293
 DB 721 CTGAATGAAAGAGATGTATATATTGAGATGTTGGGAAAGAAATGATCGATCTTAAT 780
 QY 294 IleAspValThrIleAsnGlnSerIleSerHisSerArgThrGluAspGluThrArgThr 313
 DB 781 ATA-----CATGAAGAGAAAGAAATGAATTAATGACT 813
 QY 314 -----GlnIleLeuSerIleLysLysValThrSerGluAsp 325
 DB 814 CCAGAAAGCAATATGCAATCTTCAAAAGATTAAGAAATTAATGCGTGAAGACAT 873
 QY 326 LeuLysArgSerTYrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAla 345
 DB 874 CTAAATGTTTATATATATGCACTGTGGCCACGAGGAGACAGACACCAAAAGCTTC 933
 QY 346 LysValLysGlnLys-----ValProAlaProArgTYrThrValGluLeu 360
 DB 934 ATCTTGCTGAGAAAGACAGACATGCGCTGATATCCAGGCCAGCTTTCACA----- 984
 QY 361 AlaCysGlyPheGlyAlaThrValLeuLeu-----ValValIleLeuIleValVal 377
 DB 985 ---AGAGAAATGATCATATGCTGTTTGAATCTTGCGGAGATGCTGCTAGTGAAGCTG 1041
 QY 378 TYrHisValTYrTrpLeuGlnMetValLeuPheTYrArgAlaHisPheGlyThrArgGlu 397
 DB 1042 TGTGTCAATTATAGAGTTGACTGTGTTCTATATTTATAGCAATTATTAACAGAAAGATGAA 1101
 QY 398 ThrIleLeuAspGlyLysGluTYrAspIleTYrValSerTYrAlaArg----- 413
 DB 1102 ACATTTAACAGATGAAACATATATATGCTTTGTGTCTTAACCTTAAGAAAGCCGACTT 1161
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Db 1162 GAAATGAGAGAGACACCTTTCTGTCGATTTTCCAGGGTGTGGAGAAACAT 1221
Qy 433 PheGLYTrpLysLeuCySIIlePheAspArgSerLeuProGLYGLYAsnThrValGlu 452
Db 1222 TTTGGATATAGATTATCATATTTTGAAGAGATTTAGCTTGAGAGAGCTTTGTGAT 1281
Qy 453 AlAValPheAspPheIleGlnSerArgArgMetIleValIleLeuSerProAspTyr 472
Db 1282 GAATTCACCTCAGTATGAGAGAAAGCCGAAAGCTATCATGTCCTTAAGTAAAGTAT 1341
Qy 473 ValThrGluLysSerIleSerMetLeuGluPheLysLeu--GlyValMetCysGlnAsn 491
Db 1342 ATGCTAATAGGTGACGATATGAACTTGAAAGTGCATGCAAGACATTTGCTGTAAGA 1401
Qy 492 SerIleAlaThrLysLeuIleValGluTyrArgProLeuGluHisProHis----- 509
Db 1402 AAAATT-----AAAATAATCTTAATTGAATTACACCTGTACTGACCTTCACATTTCTG 1455
Qy 510 ProGLYIleLeuGlnLeuLysGluSerValSerPheValSerThrLysGluLysSer 529
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Qy 530 LysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeu 549
Db 1516 CTTTCTTATTAAGTCAAGGTTCTGGAAGACCTTCTTACTTAATATGCTTGAAGAAACAGTC 1575

RESULT 8
US-09-110-618-1
; Sequence 1, Application US/09110618
; Patent No. 6090918
; GENERAL INFORMATION:
; APPLICANT: Parnet, Patricia et al.
; TITLE OF INVENTION: Receptor Designated 2F1
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/110,618
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,333
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2619
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hu2F1

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1626
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..1623
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..57
US-09-110-618-1

Alignment Scores:
Pred. No.: 8,48e-45 Length: 1626
Score: 528.00 Matches: 174
Percent Similarity: 46.03 Conservative: 93
Best Local Similarity: 30.00% Mismatches: 215
Query Match: 14,398 Indels: 98
DB: Gaps: 27

US-10-061-727-2 (1-687) x US-09-110-618-1 (1-1626)
Qy 4 LeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAlaSerGluArg 23
Db 28 CTTTGGGTGCTTATATCTGTA-----ACACTGCGAAGTCT 63
Qy 24 CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
Db 64 TGT-----ACTTCAGTCCCACTATCTGTGTGTAAGGGAACT 105
Qy 43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
Db 106 TTCTATCTGAACAATGTC-----TCGTGTGACTTGCA 138
Qy 62 HisSerAlaGlyLeuThrLeu---IleTrpTyrTrpThrArgGlnAspArgSerLeuGlu 80
Db 139 CATGAGATTGAAACCAACCAAGAGCTGTACAAAAGCAGTGCATCAGGAACATGTG 198
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 199 GAG---CTGAACCCAAAG---AGTTCTCGAGAAATTCCTTGCATGATGTGTTTGAG 252
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 253 TTTTGGCAGATGAGTGAATGACAGAGATCTTACTTTTCCAAATGAATAATTAATCT 312
Qy 121 TyrCysSerLysValAlaPheProLeuGluValGln-----LysAspSerCysPhe 138
Db 313 CAG-----AAATGAATTAATAATGTCATCAGAAATAAACAAGCTGTTTC 360
Qy 139 Asn-----SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154
Db 361 ACTGAAGACAGTAACTAATAAATTTGGAAGTTAAATAATTTT-----408
Qy 155 IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThr 174
Db 409 -----CAGATAACCTGTGAANC-----AGTTACATCAACACAGCTCAACAGACA 456
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Qy 194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213
Db 514 AAGAGAACGCCAGATT-----GAAATCAAGGATATTTCTCTCGGTG 558
Qy 214 ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 233
Db 559 CATTCCTTATCATATATGAGAAACTATTAATATATCCAAACCTTCATATATACATA 618
Qy 234 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisValVal 253
Db 619 GTGGAAGATGACAGTATATAGTTCGGTTCCTTCTGGAACCAAGCTTAACATGATGCA 678

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[illegible]

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1 ADDRESS: Kathryn A. Anderson, Immunex Corporation
2 STREET: 51 University Street
3 CITY: Seattle
4 STATE: WA
5 COUNTRY: USA
6 ZIP: 98101
7
8 COMPUTER READABLE FORM:
9
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: Apple Macintosh
12 OPERATING SYSTEM: Apple 7.1
13 SOFTWARE: Microsoft Word, Version 5.1a
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09/578,178
16
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 09/110,618
21
22 FILING DATE:
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Anderson, Kathryn A.
25 REGISTRATION NUMBER: 32,172
26 REFERENCE/DOCKET NUMBER: 2619
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (206) 587-0430
29 TELEFAX: (206) 233-0644
30
31 TELEX: 756822
32 INFORMATION FOR SEQ ID NO: 1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 1626 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: cDNA
39 HYPOTHETICAL: NO
40 ANTI-SENSE: NO
41 IMMEDIATE SOURCE:
42 CLONE: huzf1
43
44 FEATURE:
45 NAME/KEY: CDS
46 LOCATION: 1..1626
47
48 FEATURE:
49 NAME/KEY: mat_peptide
50 LOCATION: 58..1623
51
52 FEATURE:
53 NAME/KEY: sig_peptide
54 LOCATION: 1..57
55
56 US-09-578-178-1
57
58 Alignment Scores:
59 Pred. No.: 8,48e-45 Length: 1626
60 Score: 528.00 Matches: 174
61 Percent Similarity: 46.03% Conservative: 93
62 Best Local Similarity: 30.00% Mismatches: 215
63 Query Match: 14.39% Indels: 98
64 DB: 4 Gaps: 27
65
66 US-10-061-727-2 (1-687) x US-09-578-178-1 (1-1626)
67
68 Oy 4 LeuTPCySValValSerLeuTYrPhetyGlyLeuGInserAspAlaSerGluArg 23
69 |||||
70 :|||:|||||:
71 Db 28 CTTGGGCTGCTTAATCTGTA-----AGACCTGCAGAACTT 63
72
73 Oy 24 CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
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75 :|||:|||||:
76 Db 64 TGT-----ACTTACAGCTCCACACTTACTGTCGTGAAGGGAACT 105
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78 Oy 43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTYrSerThrAla 61
79 |||||
80 :|||:|||||:
81 Db 106 TTTATCTGGAACACTTGC-----TCGTGTCACCTTGCA 138
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83 Oy 62 HisSerIleArgIleuThrIleu---IleTrpTYrTrpThrArgIleAspArgAspLeuGlu 80
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85 :|||:|||||:
86 Db 139 CATGAGATTGAACACCAACCAAGCTGGTACAAAAGCATGAGTACACAGAAACATGTG 158

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STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/173,151A
 FILING DATE: 14-OCT-1998
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-NOV-1997
 APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998
 APPLICATION DATA:
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998
 APPLICATION DATA:
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196
 TELEFAX: (650)496-1200
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2314 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 109..1905
 US-09-173-151A-9
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 Pred. No.: 4.18e-41 Length: 2314
 Score: 495.00 Matches: 181
 Percent Similarity: 44.25% Conservative: 127
 Best Local Similarity: 26.01% Mismatches: 288
 Query Match: 13.49% Indels: 104
 DB: 4 Gaps: 27
 US-10-061-727-2 (1-687) x US-09-173-151A-9 (1-2314)
 QY 11 TyrPheTyrlYleuGlnSerAspAlaSerGluArgCysAspAspTrpGlyLeuAsp 30
 DB 128 TATTTCCTTGGCTTGTGACGAG-GAGCGAATTAAAGATTAAATTTCAGGTGTTCC 186
 QY 31 ThMetArgGlnIleGlnValPhe-----GluAspGluProAlaArgIleCysCys 47
 DB 187 ACAGAAAAACCTCCTTGAGCATATTCTACAGAGAGAGAGAAATTGCTTATTTGT 246
 QY 48 ProLeuPheGlu-----HisPhe----- 53
 DB 247 GATTTACAGAGCCACAGAAATCATATTCTGACAGAAATGAGTCTTACCAAAACAA 306

QY 54 -----LeuLysPheAsnTySerThrAlaHisSerAlaGlyLeuThrLeuIle 69
 DB 307 GTCCCTGACGACCTGCCCTTCAATGGGTAGTAACGACTTACT-----GATGTCCAA 357
 QY 70 TrpTyrlTrpThrArgGlnAspArgLeuGluGlnProIleAsnPheArgLeuProGlu 89
 DB 358 TGGTACCACCAACCTTCGATGAGATGCAATTAGAGACATTAGAGAAAGCTATCTCT 414
 QY 90 AsnArgIleSerLysGlnLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109
 DB 415 ---CAATCTTACAGACAAATGATCTTCACTTTTACACCCAGGGGTGAATATTCT 471
 QY 110 GlyAsnTyrlThrCys-----MetLeuArg-----AsnThrThrTyrlCysSer 123
 DB 472 GGGCATATATTGTTGACACCAAGATGATTAAAGCCCTTATGATGATGATGATGATGAT 531
 QY 124 LysValAlaPheProLeuGlnValValGlnLysAspSerCysPheAsnSerProMetLys 143
 DB 532 AAGATGATTTTACAGAGTAAAGTCCCGACAAATGCAATCTGTGAGTATTCGCCATCA 588
 QY 144 LeuProValHisLysLeuTyrlIleGluTyrlGly-----IleGlnArgIleThrCysProAsn 162
 DB 589 -----CATAGCAAGACCTTACTTCTGGAGACATGGCTCTATTTCTTCCGCCAGT 639
 QY 163 ValAspGlyTyrlPheProSerSerValLysProThrIleThrTrpTyrlMetGly----- 180
 DB 640 CTCAGCGCCCA---AGTATGACCAAGATCCAGCGGTAACTCGTACCAAGATGAGAAA 696
 QY 181 CysTyrlLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 DB 697 CTCCTCTCTGTGAGAAAGAGCAACCGAATCGTAGAGTAAAGTT----- 741
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrlThrCysValValIleThrTyrlProGluAsnGly 220
 DB 742 -----TATCATATACACAGGCGACATATGATGATGATGATGATGATGATGATGAT 795
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 DB 796 AGTTTCGACACACTCAGAGCTGTGTTCAAGTAGAGAACCATGTTGGAGACACTAAACTC 855
 QY 241 ValProProValIleHisSerProAsnAspHisValValTyrlGluLysGluProGlyGlu 260
 DB 856 AAACCAAGATATCTGATCTGATCTGCGAGAC-----ACATGGAAGTACCACTTGGAAG 909
 QY 261 GluLeuLeuIleProCysThrValTyrlPheSerPheLeuMetAspSerArgAsnGluVal 280
 DB 910 CTTTAACTATTAGCTGCAAGACGATTTGCTTGAAGAGGCTTTAACTGTACATA 969
 QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 DB 970 AATGTGATCATC-----AAGATCTGACCTGAGTGGAGTCTGACGATCACTGAG 1020
 QY 301 SerIleSer---HisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 319
 DB 1021 GCGAAAGATTTAAATCCACTTAAAGATGAATCATGAGGTAAATCATCTTGGA 1080
 QY 320 LysValIleSerLysLeuLysAspSerTyrlValCysHisAlaArgSerAlaLysGly 339
 DB 1081 AAGTCACTCAGCGGTATCTGCGAGGAAGTTGTTGCTTGTCCAGAACTCCATTGGA 1140
 QY 340 GluValAlaLysValAlaLysValLysGlnLysValProAlaProArgTyrlThrValGlu 359
 DB 1141 AACCAACCAAGCTCCGTCACACTGAAAGAAAG-----AGAGAGTGTGTCTC 1188
 QY 360 LeuAlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIle-----ValVal 377
 DB 1189 CTGTACATCTGTGCTGGACCATCGGACCTGTGTGGCGGTGCGGCGAGTGTCCCTC 1248
 QY 378 TyrlHisValTyrlTrpLeuGluMetValLeuPheTyrlArgAlaHisPheGlyThrAspGlu 397
 DB 1249 CTCACAGGACACTGATGATGAATATGCTGCTGTACCGGACCTACCAAGCAAGCAAGATCAG 1308
 QY 398 ThrIleLeuAspGlyLysGluTyrlAspIleTyrlValSerTyrlAlaArg----- 413

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DB 1309 ACCGTTGGGATTAAGGATTTGATGCTTGTATCTCAATGCAAAATGAGCTCTTTT 1368
QY 414 -----AanAlaGlugluGluGluPheValLeuThrlLeuArgGly 427
DB 1369 CCAAGTGAAGCCACTTATCTCTGAGTGAAGAACACTTGGCCCTGAGCCCTATTTCCTGAT 1428
QY 428 ValLeuGluGluGluPheGlyTyrTyrLeuGluGluPheAspArgAspSerLeuProGly 447
DB 1429 GTTTTGAAGAAACAAATATGATATAGCTGTGTGTTGCTGTAAGAGATGTGGCTCCAGGA 1488
QY 448 GluAsnThrValGluAlaValPheAspPheLeuGluArgSerArgGlyMetLeuVal 467
DB 1489 GGAGTGTATGCAAGACATTTGACATTTATTAAGAGAACAGAACAGAAATATTATTC 1548
QY 468 LeuSerProAspTyrValThrGluSerLeuSerMetLeuGluPheGlyVal 487
DB 1549 TTATGCCCCCACTATGATTCAGACCCAGTATCTTTGACCTACAGACAGATGAAATCTT 1608
QY 488 MetCysGluAsnSerLeuAlaThrTyrLeuLeuValGluTyr-----Arg 503
DB 1609 GCCTTGATGATCA---ACACTGAAATCATTTTATTAAGTTCTGTACTTCCAGAG 1665
QY 504 ProLeuGluHisProHisProGlyLeuGluLeuGluSerValSerPheValSer 523
DB 1666 CCAGAGCTCTTACTCATCTC---GTGAAAAAAGCTCTCAGGGTTTGGCCACAGTTACT 1722
QY 524 TrpLeuGluGluLeuSerTyrHisSerGlySerLeuPheThrPheValLeuArgLeuAla 543
DB 1723 TGAAGAGGCTTAATAATCACTTCTCCCAATTTAGGTTTGAGCCAAATGACGCTACAC 1782
QY 544 LeuProLeuArgSerLeuSerAlaSerSerGlyTyrAsnGluSerCysSerSerGlnSer 563
DB 1783 ATCCCTGTGAAAAAC---TCTCAGGAGATTCAGTGAACAGCAGCTCAGAAATTAATCTAG- 1838
QY 564 AspGluSerLeuAspHisValGluAlaGArgArgSerArgLeuGluProProGluLeu 583
DB 1839 GATTTTTCAGTGAAGAGACTCAGTAGAACAGAACACACGAGAGAGCT-CCAGGCTTA 1897
QY 584 GlnSerSerGluArgAlaAlaGlySerPro-----ProAlaProGly**MetSerLys 601
DB 1898 AGGAATGCTGAATGAGCCCTGAGGCCCTCCAGTCCAGTCCCTGGG---ATAGAGATG 1954
QY 602 HisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyGluAsn 621
DB 1955 TT-GCTGACAGAGAACTCAGCTGTGTGTGTGTCTTC-----1992
QY 622 HisLeuArgAsnLysSerArgAlaGluLeuHisAsnGlnProGlnThrHisLeu 641
DB 1993 AGGCTGATAGGAATTCAAAGAGCTCTCTG-----2022
QY 642 CysLysProValProGlnGluSerGluThrGlnTrpIleGlnAsnGly 657
DB 2023 -----CCAGCACCAAGCAAGCTTGAATGACAAATG-----AATGGG 2058

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COMPUTER READABLE FORM:
MEDIAN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/821,716
FILING DATE: 19920114
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 125627
FILING DATE: 25-NOV-1987
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 160550
FILING DATE: 25-FEB-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 258756
FILING DATE: 13-OCT-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 691551
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2001-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2356 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
IMMEDIATE SOURCE:
LIBRARY: MOLLIR
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1955
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 282..1952
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..281
US-07-821-716-3
Alignment Scores:
Pred. No.: 2,04e-40 Length: 2356
Score: 488.50 Matches: 175
Percent Similarity: 43.21% Conservative: 121
Best Local Similarity: 25.55% Mismatches: 254
Query Match: 13.31% Indels: 136
Gaps: 31
US-10-061-727-2 (1-687) x US-07-821-716-3 (1-2356)
QY 34 GlnIleGlnValPheGluAspGluProAlaArgIle-----45
DB 285 GAGATTGACGTATGTCAGAAATATCCAAATCAGATCTTTGTTTATCTGTAATGAA 344
QY 46 -----LysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
DB 345 ATTGATATTGCAAGTGTCTTACTCAATAAATGACAC-----386
QY 62 HisSerAlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGluGlu 81
DB 387 -----GGGACACCAATATTGCTAC-----AAGAAATGACAGCAAGACC 425

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QY 82 ProIleAsnPhenArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrpPhe 101
 DB 426 CCCATTCACGGAC---CGGACCTCCAGGATTCATCAGAGAAATGAAACATCTTGTTGTT 482
 QY 102 ArgProThrLeuLeuAsnAspThrGlyAsnTrpThrCysMetLeuArgAsnThrTrp 121
 DB 483 GTACCTCCAGAGGTGAGAGACTCAGATATTTACTATTGTATGTAAGAACTCACTTAC 542
 QY 122 CysSerLeuValAlaPheProLeuGluValAlaGlnLysAspSer-----CysPheAsn 139
 DB 543 TECTCAAACTAAAGTAACCGTAAGTGTGTTGAGAAATGACCTGCTGTGTTCACG 602
 QY 140 SerProMetLysLeuProValAlaHisLysLeuTrpIleGluTrpIleGlnArgIleThr 159
 DB 603 ACACAGGCCACCTTCCCA---CAGCGCTCCACATTGCC---GGGATGGAACCTCTGG 656
 QY 160 CysProAsnValAspGlyTrpPhe-----ProSerSerValLysProThrIleThrTrp 177
 DB 657 TCCCTTATGTG---AGTTATTTTAAAGATGAAATATATCATGTTACCCGAGCTCCAGTGG 713
 QY 178 TyrMetGlyCysTrpLysIleGlnAsnPhenAsnValIleProGluGlnMetLeu 197
 DB 714 TATTAAGACTGT---AAACCTCTGCTTTTGACACAGTGTGCTTTCCGAGTAAAGAT 770
 QY 198 SerPheLeuIleAlaLeuIleSer-----AsnAsnGlyAsnTrpThrCysValValThr 215
 DB 771 AAACGTCTGTAGAAATGTGCTGAAGACACAGAGGGGACATATATGTCCTGATGTC 830
 QY 216 TyrProGluAsnGlyValArgThrPheHisLysLeuThrArgThrLeuThrValLysVal 235
 DB 831 TATACCTTCCGGGGGAAGCAATATCCGCTCACAGAGTAAATCAATTTATCAACATAGAT 890
 QY 236 SerProLysAsnAlaValProValIleHisSerProAsnAspHisValValTrpGlu 255
 DB 891 GAAACAAAGAGGAC---AGACCTGTATCTGAGCCCTCGAATAGACATC---GAA 944
 QY 256 LysGluProGluGluGluLeuLeuIleProCysThrValTrpPheSerPheLeuMetAsp 275
 DB 945 GGTGACCCAGGATCATGATGATACAACTGATCTGACGTCCAGGCCAGTTC----- 995
 QY 276 SerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAsp 295
 DB 996 ---TCAGACTTGTCTACTGAGAGTGAATGATCA-----GAA 1031
 QY 296 ValThrIleAsnGluSer-----IleSerHisSerArgThr 307
 DB 1032 ATTTGAATGAAATGATCATTTCTAGCTGAGACTCATCATTTTGTGAACATCTTCAACC 1091
 QY 308 GluAspGlu---ThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeu 326
 DB 1092 AAAAGAAATACACCTCATTAACAACCTTAACAGTTCAGAGATTAAGGCCAGTTTAT 1151
 QY 327 LysArgSerTrpValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaLys 346
 DB 1152 CGCTATCCGTTATCTGTGTGTTAAGAACAC---AATATTTTGTAGTGGGGCAT 1205
 QY 347 ValLysGlnLysValProAlaProArgTrpThrValGluLeuAlaCysGlyPheGlyAla 366
 DB 1206 GTGCGATTATATATACCCAGCTCCGCTCACTCAAGAAATTAATCTCGGGGCTTATCATC 1265
 QY 367 ThrValLeuLeuValValIleLeuIleValValTrpHisValTrpLeuGlnMetVal 386
 DB 1266 CTCACGGCTACAAATGTATGCTGTGTGATCATATTAAGCTTCAAGGTGACATAGTG 1325
 QY 387 LeuPheTrpArgAlaHisPheGly-----ThrAspGluThrIleLeuAspGlyLysGlu 404
 DB 1326 CTTTGTACAGGAGACTCGCTCGTTTCTTCCTTCAAAAGCTTCAGATGGAAGAC 1385
 QY 405 TyrAspIleTrpValSerTrpAlaArgAsnAlaGluGlu-----Glu 418
 DB 1386 TAGATGCTATATTTCTTTATCCAAAGACCTCGAGAGGGGTCTTTCAGACTTAGAT 1445

QY 419 GluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTrpLysLeuCys 438
 DB 1446 ACTTTGTGTTTAACTGTGCTGAGCTCTTGAGAGGACAGTTTGATTAACAAGCTGTT 1505
 QY 439 IlePheAspArgAspSerLeuProGluGlyAsnThrValGluAlaValPheAspPheIle 458
 DB 1506 ATTTATGAAAGGATGACTATGTTGGAGAAATACCATGAGGTTTCTATATGAAATGTA 1565
 QY 459 GlnArgSerArgArgMetIleValValLeuSerProAsp----- 471
 DB 1566 AAGAAAGAGAGAGCTGATTTATCTTATGAGAGATATGAGAGCTTACGCTGGCTG 1625
 QY 472 ---TyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
 DB 1626 GCCAGATCTCGAAGAGCAATAGCCATA-----TACATGCTTCATCCAG 1673
 QY 491 AsnSerIleAlaThrLysLeuIleValAlaGluTrpArgProLeuGlu-----HisPro 508
 DB 1674 GAAGAAAT---AAATCTCTGCTGTGAGTTGAGAAATTCAGACTATGAGAAA 1727
 QY 509 HisProGlyIleLeuGln---LeuLysGluSerValSerPheValSerTrpLysGly--- 526
 DB 1728 ATGCCGATTCATTTCAATGATTAAGCAAGAAACAGGACTATTTGCTGTGACGAGAC 1787
 QY 527 ---GluLysSerLysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeu 544
 DB 1788 TTTCAAGAAAGACACAGCTGCAAGACAGGCTCTGAGAAAATTAAGATACAGATG 1847
 QY 545 ProLeuArgSerLeuSerAlaSerSerGlyTrpAsnGluSerCysSerSerGlnSerAsp 564
 DB 1848 CCA----- 1850
 QY 565 IleSerLeuAspHisValGlnArgArgSerArgLeuLysGluProProGluLeuGln 584
 DB 1851 ---GCCACAGAAATCACCTG----- 1871
 QY 585 SerSerGluArgAlaAlaGlySerProProAlaProGly**MetSerLysHisArgGly 604
 DB 1872 TCTAAACCGCTTACTAACCTGATCTGTGCGGAGACCTAAGAGAAACT-GCCGCG 1930
 QY 605 LysSerSerAlaThrCysArgCysCysValThrTrpCysGluGluGluAsnHisLeuArg 624
 DB 1931 AGCAACACCTTACCACTCGGCTGACATGCAAAAGTGGGACAGCCAA---GAATTCGG 1987
 QY 625 AsnLysSerArgAlaGluIleHisAsnGlnProGln----- 636
 DB 1988 AATATCTCCAT-----CATTAAGAGCTGCACTGGGCTGTGCTCCAGTAAAC 2038
 QY 637 ---TrpGluThrHisLeuCysLysPro--ValProGlnGluSerGluThrGlnTrpIleG 655
 DB 2039 AGTCAGAAACCAAACTGTGCACTCCCTTGTCCAGATCACTGGAACCTGAGTGGAG 2098
 QY 655 LysAsnGlyThr 658
 DB 2099 AGAACAGGACT 2109

RESULT 13
 US-08-381-603-3
 Sequence 3, Application US/08381603
 Patent No. 5858355
 GENERAL INFORMATION:
 APPLICANT: Glorioso, Joseph C.
 APPLICANT: Evans, Christopher H.
 APPLICANT: Robbins, Paul D.
 TITLE OF INVENTION: Gene transfer for treating a connective tissue of a
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eckert Seamans Cherin & Mellott
 STREET: 1700 Market Street Suite 3232
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA

```

      ZIP: 19103
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent in Release #1.0, version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/381,603
      FILING DATE:
      CLASSIFICATION: 514
      ATTORNEY/AGENT INFORMATION:
      NAME: Gould, Jr., Lewis F.
      REGISTRATION NUMBER: 25,057
      REFERENCE/DOCKET NUMBER: 109070-11
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (215) 575-6000
      TELEFAX: (215) 575-6015
      TELEX: 866172
      INFORMATION FOR SEQ ID NO: 3:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1782 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      HYPOTHEICAL: NO
      ANTI-SENSE: NO
      IMMEDIATE SOURCE:
      LIBRARY: Mouse T-cell cDNA library
      CLONE: Mouse Interleukin-1 Receptor
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 46..1776
      US-08-381-603-3

Alignment Scores:
  Pred. No.: 3,276-40      Length: 1782
  Score: 484.50           Matches: 153
  Percent Similarity: 46.04%      Conservative: 120
  Best Local Similarity: 25.80%    Mismatches: 225
  Query Match: 13.21%           Indels: 95
  DB: 2                      Gaps: 27

US-10-061-727-2 (1-687) x US-08-381-603-3 (1-1782)
  QY 34 GlnIleGlnValPheGluAspGluProAlaArgIle----- 45
  DB 106 GAGATTGACGTATGTACAGATATCCAAATCAGATCGTTTGTATTATCTGTAATGAA 165
  46 -----LysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
  166 ATGATATTGCGCAAGTGTCTTACTCCAAATATAAATGAC----- 207
  QY 62 HisSerIleGlyLeuThrLeuIleTyrTyrThrArgIleAspArgAspLeuGlu 81
  DB 208 -----GGCGACACCATATATTGGTAC-----AAGATGACAGCAAAACC 246
  QY 82 ProIleAsnPheArgLeuProGluAsnArgIleSerIleGluLysAspValLeuTyrPhe 101
  DB 247 CCCATATACACCGGAC---CGGAGCTCCAGATCATCATGACGAGATGAACATCTTGGGTTT 303
  QY 102 ArgProThrIleLeuLeuAsnProThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyr 121
  DB 304 GATCTGCGCAAGGTGAGAGACTCAGATATATCTATGTATAGTAAGAACTCAACTTAC 363
  QY 122 CysSerIleValAlaPheProLeuGluValValGlnLysAspSer-----CysPheAsn 139
  DB 364 TGCGTCAAAACTAAAGTAACCGTAACTGTGTAGAGATGACCCGTGGCTGTGTACAGC 423
  QY 140 SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThr 159
  DB 424 ACACAGGCAACCTTCCCA---CAGCGGCTCCACATGTCC---GGGATGGAAGCTTGTG 477

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  QY 160 CysProAsnValAlaSpGlyTyrPhe-----ProSerSerValLysProThrIleThrTyr 177
  DB 478 TGCCCTTATGTC---AGTATATTTAAAGTAAATTAATGATGATACCGAGGTCCAGTGG 534
  QY 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGluLysMetAsnLeu 197
  DB 535 TATTAAGAACTGT---AAACCTGTGCTTTCAGCAACGTAGAGCTTTCGAGATTAAGAT 591
  QY 198 SerPheLeuIleAlaLeuLeuSer-----AsnAsnGlyAsnTyrThrCysValValThr 215
  DB 592 AAACGTGTGTGAGAGATGTGCTGTAAGACACAGAGGAGACTATATATATCCGTATGTC 651
  QY 216 TyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGly 235
  DB 652 TATAGCTCCGGGGGAGAGCAATATCCGTCACACAGATATATCAATTATCAATATAGAT 711
  QY 236 SerProLysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGlu 255
  DB 712 GAAACAGAGAGGAGAC---AGACCTGTATCTGAGGCCCTCGGAAATGAGACGATC---GAA 765
  QY 256 LysGluProGlyGluGluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAsp 275
  DB 766 GCTGACCCAGAGATCAATGATACACTGATCTGACACGTACGCGCCAGTTC----- 816
  QY 276 SerArgAsnGluValTyrThrThrIleAspGlyLysLysProAspAspIleThrIleAsp 295
  DB 817 ---TCAGACTTGTCTACTCGAAGTGAATGATCA-----GAA 852
  QY 296 ValThrIleAsnGluSer-----IleSerHisSerArgThr 307
  DB 853 ATGAATGGAATGATGATTCATTTCTAGCTGAAGACTATCAATTGTGGAAATCTTCAACC 912
  QY 308 GluAspGlu---ThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeu 326
  DB 913 AAAAGAAATATACACTCTATACACACTTAAACATTTCAAGAGTTAAAGCCAGTTTAT 972
  QY 327 LysArgSerTyrValCysHisAlaArgSerAlaLysGlyValAlaLysAlaLys 346
  DB 973 CGGTATCCGTATATCTGTGTGTGTAAAGACAC---AATATTGTGACGCGGCAT 1026
  QY 347 ValLysGlnLysValProAlaProArgTyrThrValGlnLeuAlaCysGlyPheGlyAla 366
  DB 1027 GTGCAGTATATATACCCAGCTCCCTGACTTCAAGAAATTACCTCATCGGCGCTTATCATC 1086
  QY 367 ThrValLeuLeuValValIleLeuIleValValTyrHisValTyrThrLeuGluMetVal 386
  DB 1087 CTCACGGCTTACAAATGTGTATGCTGTGTGTCATCTTAATAAGCTTCAAGGTGACATAGT 1146
  QY 387 LeuPheTyrArgAlaHisPheGly-----ThrAspGluThrIleLeuAspGlyLysGlu 404
  DB 1147 CTTTGGTACAGGACCTCCGTCTGCTTTCTTCCCTTCAAAAGCTTCAATATGAAAAAGACA 1206
  QY 405 TyrAspIleTyrValSerTyrAlaArgAsnAlaGluGlu-----Glu 418
  DB 1207 TACAGATGATATATTTCTTATCCCAAGACCTCGGAGAGGGGCTCTTCCAGACTTAGAT 1266
  QY 419 GluPheValLeuLeuThrLeuArgGlyValLleuGluAsnGluPheGlyTyrLysLeuCys 438
  DB 1267 ACTTTGTTTAAACGTGTTCGAGGCTTGAGGTCCTTGAGAGGACAGTTTGAATCAAGCTGTC 1326
  QY 439 IlePheAspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIle 458
  DB 1327 ATTATGGAAGGATACATGTGTGGAAGAAATACATGAGGTTTACTAATAAATATGA 1386
  QY 459 GlnArgSerArgArgMetIleValValLeuSerProAsp----- 471
  DB 1387 AAGAAAGACAGAGGCTGATTTATCATTTAGTGAAGATATGAGAGCTTCAAGCTGCTG 1446
  QY 472 ---TyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
  DB 1447 GGCACACTCATCTGAAGAAATAGCCATA-----TCAATGCTCATATCCAG 1494
  QY 491 AsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGlu-----HisPro 508

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Db 913 AAAAAAATACACCTTACACACTTACACTTAAAGCCAGTTTAT 972
Qy 327 LysArgSerTyrValGlySerHisAlaArgSerAlaGlyGluValAlaAlaAlaAla 346
Db 973 CGCTATCCGTTTATCTGTTGTTGTTGAAGACACA-----AAATTTTGTGAGTCGGGCAAT 1026
Qy 347 ValLysGlnLysValProAlaProArgTyrThrValGlnLeuAlaGlySerGlyPheGlyAla 366
Db 1027 GAGCAGTTATATATACCAAGCTCCCTGACTTCAAGAAATTAATTAATTCGAGGCTTATATC 1086
Qy 367 ThrValLeuLeuValValLeuLeuValValTyrHisValTyrThrPheLeuGlnMetVal 386
Db 1087 CTCACGGGCTACATTTGATAGCTGCTGTGTGATCATATTAAGTCTTCAAGGTGACATAGTG 1146
Qy 387 LeuPheTyrArgAlaHisPheGly-----ThrAspGluThrIleLeuAspGlyLysGlu 404
Db 1147 CTTTGGTACAGGAGCTCTGCTGCTGTTTCTTCCCTTCAAAAGCTTCAGATGAAAGACA 1206
Qy 405 TyrAspIleTyrValSerTyrAlaArgAlaGlnGlu-----Glu 418
Db 1207 TACGATGCAATATATCTTTATATCCCAAGACCCTGGAGAGGGGCTCTTTCAGACTTAGAT 1266
Qy 419 GluPheValLeuLeuThrIleuArgGlyValLeuGlnAsnGlnPheGlyTyrLysLeuCys 438
Db 1267 ACTTTGTTTAAACTGTTGCTGCTGAGCTTTCGAGGAGACATTTGATCAAGCTGTTTC 1326
Qy 439 IlePheAspArgAspSerLeuProGlyGlyAsnThrValGlnAlaValPheAspPheIle 458
Db 1327 ATTATGGAAGGAGATCATATGTTGGAGAAATATACATCGAGGTTACTATATGAAATGTA 1386
Qy 459 GlnArgSerArgArgMetIleValValLeuSerProAsp----- 471
Db 1387 AAGAAAAGCAAGAGGCTGATTAATCATTTAGTAGAGATATGAGAGGCTTCACTGCTG 1446
Qy 472 ---TyrValThrGlnSerIleSerMetLeuGlnPheLysLeuGlyValMetCysGln 490
Db 1447 GCGCACTCATCTAGAGCAAAATAGCCATA-----TACATGCTCATATCCAG 1494
Qy 491 AsnSerIleAlaThrLysLeuIleValGlnTyrArgProLeuGlu-----HisPro 508
Db 1495 GAAGGAAT-----AAATCGTCTGCTGAGTGGAGAAATCCAAAGACTATAGAAA 1548
Qy 509 HisProGlyIleLeuGln---LeuLysGlnSerValSerPheValSerTyrPheLysGly 526
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Db 1609 TTTCAGAAAGACACACAGCTGTCAGAAAGACAGGTTCTGGAAAACTTAAATACACAGATG 1668
Qy 545 ProLeuArgSerLeuSerAlaSerSerGlyTyrAsnGlnLysCysSerSerGlnSerAsp 564
Db 1669 CCGAGCCACACGAGATCA-----CCATTTGCTTAAACACCGCTTA 1707
Qy 565 IleSerLeuAspHisValGlnArgArgSerArgLeu 577
Db 1708 CTAACTTGATCTCTGCGGACACTAAGAGAAACTG 1746

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STREET: 1700 Market Street Suite 3232
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,212
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/027,750
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEFAX: (215) 575-6015
TELEX: 866172
INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1782 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
LIBRARY: Mouse T-cell cDNA library
CLONE: Mouse Interleukin-1 Receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 46..1776
US-08-685-212-3
Alignment Scores:
Pred. No.: 3.27e-40 Length: 1782
Score: 484.50 Matches: 153
Percent Similarity: 46.04% Conservative: 120
Best Local Similarity: 25.80% Mismatches: 225
Query Match: 13.21% Indels: 95
DB: Gaps: 27
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Qy 62 HisSerAlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGlnGlu 81
Db 208 -----GGGACACCACTAATTTGGTAC-----AAGAAATGACGCAAGACC 246
Qy 82 ProIleAsnPheArgLeuProGlnAsnArgIleSerLysGlnLysAspValLeuThrPhe 101
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Qy 102 ArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrTyr 121
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 Qy 160 CysProAsnValAspLeuTyrPhe-----ProSerSerValLysProThrIleuThr 177
 Db 478 TCCCTTATATGTC---AGTTATTTTAAAGATGAAATATATATAGTATCCCGAGTCCAG 534
 Qy 178 TyrMetGlyCysTyrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 197
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 Qy 198 SerPheLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 215
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 Qy 216 TyrProGluAsnGlyValArgThrPheHisIleuThrValArgThrValValVal 235
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Search completed: April 30, 2003, 13:03:13
 Job time : 93 secs

GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2003, 11:50:55 ; Search time 152 Seconds
(without alignments)

5340.616 Million cell updates/sec

Title: US-10-061-727-2

Sequence: 1 MTLMCVSLKFLGILGSDA.....SALALHRTDLSNNNDPYLL 687

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 746064 segs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=llsum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database: Published Applications NA:

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14: /cg2n_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2580	70.3	1713	9 US-10-215-211-3 Sequence 3, Appli
2	1934	52.7	9	US-10-215-211-5 Sequence 5, Appli
3	1930	52.6	2733	9 US-09-935-868-27 Sequence 27, Appli
4	825	22.5	2061	9 US-10-011-548-3 Sequence 3, Appli

5	800	21.8	1737	9 US-10-011-548-1	Sequence 1, Appli
6	767	20.9	2537	9 US-10-011-548-34	Sequence 34, Appli
7	531	14.5	287	10 US-09-864-761-32830	Sequence 32830, A
8	528	14.4	1626	10 US-09-981-421-3	Sequence 3, Appli
9	528	14.4	1626	12 US-10-157-447-1	Sequence 1, Appli
10	495	13.5	2314	9 US-10-011-548-9	Sequence 9, Appli
11	495	13.5	2681	9 US-10-212-287-6	Sequence 6, Appli
12	495	13.5	2681	10 US-09-981-421-1	Sequence 1, Appli
13	495	13.5	2752	9 US-09-731-449-1	Sequence 3, Appli
14	484.5	13.2	1782	10 US-09-731-175-3	Sequence 3, Appli
15	482	13.1	4989	10 US-09-899-980A-3	Sequence 3, Appli
16	479.5	13.1	2830	12 US-10-157-447-3	Sequence 3, Appli
17	478	13.0	1704	9 US-10-004-633-38	Sequence 38, Appli
18	471.5	12.9	1797	9 US-09-731-449-3	Sequence 3, Appli
19	463.5	12.6	2058	10 US-09-899-980A-4	Sequence 4, Appli
20	457	12.5	1686	10 US-09-775-046-14	Sequence 14, Appli
21	446.5	12.2	1845	9 US-10-212-287-1	Sequence 1, Appli
22	446.5	12.2	2259	9 US-10-011-548-15	Sequence 15, Appli
23	445.5	12.1	1833	9 US-10-011-548-13	Sequence 13, Appli
24	444.5	12.1	1689	10 US-09-775-046-12	Sequence 12, Appli
25	436	11.9	1404	9 US-10-011-548-7	Sequence 7, Appli
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28	418.5	11.4	1991	9 US-10-011-548-19	Sequence 19, Appli
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30	401	10.9	478	10 US-09-864-761-16315	Sequence 16315, A
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39	229.5	6.3	1357	9 US-10-004-633-44	Sequence 5, Appli
40	229.5	6.2	1011	9 US-09-899-980A-5	Sequence 47, Appli
41	226.5	6.2	1011	10 US-10-004-633-47	Sequence 2, Appli
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43	224.5	6.1	1659	9 US-09-977-418-17	Sequence 56, Appli
44	220.5	6.0	734	9 US-10-091-418-56	Sequence 407, Appli
45	220.5	6.0	734	10 US-09-764-853-407	

ALIGNMENTS

RESULT 1
US-10-215-211-3
; Sequence 3, Application US/10215211
; Publication No. US20030049255A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
FILE REFERENCE: 3321-A
CURRENT APPLICATION NUMBER: US/10/215,211
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/310,789
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1713
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1713)
OTHER INFORMATION:
US-10-215-211-3
Alignment Scores:
Pred. No.: 5,71e-290 Length: 1713
Score: 2580.00 Matches: 487

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Qy 161 ProAsnValAlaPglYrPheProSerSerVallyspPothrIleThrTrpYrMetGly 180
Db 481 CCAATGTAGATGATATTTTCTCCAGTCCTCAACCCAGATCACTTGTGATATGAGGC 540
Qy 181 CysTyrIleValIleGlnAsnPheAsnAsnValIleProGluGluMetAsnLeuSerPheLeu 200
Db 541 TGTATTAATAACAGATTTTAAATATATATATACCCAGAGATATGAACTTAACTTCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTCAATTAATATGAAATTAACACATGTGTGTATTAATCCAGAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValIlyValIleGlySerProIyAsnAla 240
Db 661 CGTACGTTTCATCTCACACAGACTCTGCTCTAAAGTAGAGGCTCTCAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluIlyValProGlu 260
Db 721 GTGCCCCCTGATCATTCACCTTAATGATATGCTATATGAGAAAGAACAGAGAG 780
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Db 781 GAGCTACTCATCTCCCTGACGCTATTTTATTTTCTGATGAGATTCCTCGAATGAGTT 840
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Db 1021 GTTCCCAAGCAGCCAGAGTGAACAGAAAGTGCAGCTCCAAAGTATACAGAGTG 1074

RESULT 4
US-10-011-548-3
Sequence 3, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Debets, Johannes Eduard Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kastelen, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2058
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-548-3

Alignment Scores:
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Score: 825.00 Matches: 228
Percent Similarity: 46.78% Conservative: 106
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US-10-061-727-2 (1-687) x US-10-011-548-3 (1-2061)
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DB 964 GTGGAAGCTGACCTG---GGGATTTATACCTGCCATCTTGAAACGAAATGACG--- 1017
OY 342 AlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeuAla 361
DB 1018 ---AAACATGCCAGTGTGCTTGGCGCTAAAGAGATTATCTATTAATAATTGAGCTTCA 1074
OY 362 CysGlyPheGluValThrValIleLeuValValIleLeuIleValValTyrHisValTyr 381
DB 1075 GGGGGCTGGGAGCAATCTTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134
OY 382 TrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeuAsp 401
DB 1135 AACATTGAATGATGCTCTTCTTACAGGACACCTTGAGACTGATGAATGAATGATGAC 1194
OY 402 GlyLysGluTyrAspIleTyrValSerTyrAlaArg----- 413
DB 1195 AACAAAGAAATATGATGCTATCTCTTACAAAGAGTGAACCAAGTACTTAACTAGACTGT 1254
OY 414 ---AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValIleGluLysGln 432
DB 1255 GACAAATCTGGAAGAGAGAGCTTGTCTTGAAGATGACCAAGATGCTCGGAGAAAACAC 1314
OY 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyLysAsnThrValGlu 452
DB 1315 TATGATATTAATCTTCTTATCCAGAAAGAGCTGATTTCAAGTGAAGAACTACATAGAA 1374
OY 453 AlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerProAspTyr 472
DB 1375 GATCTCACAGATATGTGTAACAAAGAGAAAGCTTATATCGTGTAACCTCCAGACTAT 1434
OY 473 ValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGlnAsnSer 492

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DB 1435 ATCTTCAGACGGGAGATGAGTAT-----TTGAACTGGAAGAGACATCCATTAACATG 1488
OY 493 IleAlaThr-----LysLeuIleValValGluTyrArgProLeuGlnHisProHis 509
DB 1489 CTAGTCAGTGAGAAATGCAAGTGAATTTGATGTAGTGTACAGAAATTAAA----- 1539
OY 510 ProGly-----IleLeuGlnLeuLysGluSerVal-----Ser 520
DB 1540 ---GGGAAAGTAAATTCGACAGAGTGAATGATCACTTAACCGTACATCAAACTTCTGTCC 1596
OY 521 PheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeu 540
DB 1597 CTGATCAAGTGAAGAGATCCAAAAGCAGCAATTAATTAATTAAGTTTGAAGCACTTA 1656
OY 541 ArgLeuAlaLeuProLeuArg----- 547
DB 1657 GTATATGAATGCCATCAAGAAAAGAAATGTAACCTCGGTGCCAGTTGTGACCTCC 1716
OY 548 -----SerLeuSerAlaSerGly 554
DB 1717 GCAGAAACAAGACTTTTGGAGAACTCCAGCTTAACCTTAATTCCTGACAGCACTACT 1776
OY 555 TrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArgArg 574
DB 1777 TCAGCCACTGTGTGTCTCATCTGACGTATCTC----- 1809
OY 575 SerArgLeuLysGluProGluLeuGlnSerSer----- 586
DB 1810 -----CCTGAATTCACCTTCAGATTCATGCAATGCAAGCACTGT 1851
OY 587 -----GluArgAlaAlaGlySerProProAlaProGly**MetSer 600
DB 1852 TGCAGAGTTATTAACATGATGATACCAAGCAGCTTCCAGATCTTCTTACGCAAC 1911
OY 601 LysHisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyGlu 620
DB 1912 CACCAT-----ACTTATTTATACCTGCCCTCTGACCTGACTCAAGGACAG 1956
OY 621 AsnHisLeuArgAsn-----LysSerArgAlaGluIleHis 632
DB 1957 CTACCCCTTAATTAACACCTCGAAAGATACCCAGATTTTCAC 1998

RESULT 5
US-10-011-548-1
; Sequence 1, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,548
; FILING DATE: 22-Oct-2001
; CLASSIFICATION: <Unknown>

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OY 142 MetLysLeuProValHisLysLeuTyrIleGluTyrGly-----IleGlnArg 157
DB 358 ATGAAG-----TATTTGAAAAGCGAAGCTTAGCAAAACCAAGAA 399
OY 158 IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177
DB 400 ATTTCATGCGGTGACATGAGATGATTTTCTTACGCCAACAGAGAACCTGAAATCCCTTGG 459
OY 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGluGluMetAsnLeu 197
DB 460 TACAGGAATGAGGACAAAACATGAGGCCAAGATGATGTTTCAAGAGAGATCTCTG 519
OY 198 SerPheLeuIleAlaLeuIleSerAsnGlnIAsnTyrThrCysValAlaThrTyrPro 217
DB 520 CTATTAAGAGAGATCAGAGAGATGACATTTGAAATTATACCTGTGAAATTAATTT 576
OY 218 GlyAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValAlaGlySerPro 237
DB 577 ---GAGGCGCTTTGTTGAGAGAACTACTGAAATTAACTGTACA-----GCCCT 624
OY 238 LysAsnAlaValProProValIleHisSerProAsnAspHis-----ValValTyrGlu 255
DB 625 CTGACTGATAGCCACCAAGCTTTGTATCTATGAAAAGTAACTGACAAATTCAGAG 684
OY 256 LysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAsp 275
DB 685 ACCAGCTGGGTGACTGCTAATCTAATCTAGCAGAGCTTTCTTGGGTACGCGAGAT 744
OY 276 SerArgAsnGluValTrpTrpThrIleAspGlyLysProAspAspIle----- 292
DB 745 GTCACTCTTTAATTACTGATGAGAGAGAAATTAATTAATGATCTGATGAAAT 804
OY 293 -----ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAsp 309
DB 805 CGAGTTGGGAAAGTACATTAAGATTT-----CTTAAGAGCATCTTGGGAGACAG 855
OY 310 GluThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeuLysArgSer 329
DB 856 GAAGTTTCCATCTCATTAAT--GTGACCTGTGAGAAAGAGACTTG---GGAAT 909
OY 330 TyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaValLysGln 349
DB 910 TACTCTCTTATGTTGAAATGAAATGAACTGCT---CGACAGCCAGGCTTCTCT 963
OY 350 LysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGluAlaThrValLeu 369
DB 964 CATTAACGAGAGCTAATGTACACAGTGAACTTCTGAGGCTTGTGCTATACTCTTG 1023
OY 370 LeuValValIleLeuIleValAlaTyrHisValTyrTrpLeuGluMetValLeuPheTyr 389
DB 1024 CTGCTTGATGTTGGTGGACCATCTACAGGTGTAACAAGATAGAAATCATCTCTTAC 1083
OY 390 ArgAlaHisPheGlyThrArgGluThrIleLeuAspGlyLysGluTyrAspIleTyrVal 409
DB 1084 AGGATCATTTTGTAGCTGAAGCTCGATGAGCAATTAAGATTTGATGACTACTTA 1143
OY 410 SerTyrAlaArg-----AsnIleGluGluGluGluPhe 420
DB 1144 TATATACCAAAATGATCTCTGACAGTGAATCAAGAGCTGGGAGAAAGACGTTTT 1203
OY 421 ValLeuLeuThrLeuArgGlyValLysGluAsnGluPheGlyTyrLysLysCysIlePhe 440
DB 1204 GCCCTTGAATCTTACTGATATGTTGAAAGCATTAATGATTAAGTTGTTATACCA 1263
OY 441 AspArgAspSerLeuProGlyLysThrValGluAlaValPheAspPheIleGlnArg 460
DB 1264 GATAGAGATTATATCCCACTGCAACATACATGAAGATGTGCAAGATGTGATGATCA 1323
OY 461 SerArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
DB 1324 AGCAAGCGGTATATATGTCAACCCCAATTAAGTATTGAAGGCGGTGAGCATC 1383

OY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThr-----LysLeu 497
DB 1384 -----TTGACCTGAAACCAAGCTTCAAAATATGCTTGTGATGAGAAATTAAGTG 1437
OY 498 IleValValGluTyrArgProLeuGlnHisProHisProGlyIleLeuGlnLeuLysGlu 517
DB 1438 ATTCTAATGAAATGACAGAACTGAGA-----GGAATTTATGAACTACCAAGAG 1485
OY 518 -----SerValSerPheValSerTrpLysGlyLys 528
DB 1486 GTGAGCGCTGAGACCAACCATCAAGCTCTGACGGTCATTAATATGATGACCAAAA 1545
OY 529 SerLysHisSerGlySerLysPheTrpLysAlaLeuAlaGlyLeuAlaLeuProLeuArg 547
DB 1546 TGCAACAAGTGAACCTCAAGTTCTGAAACGTTTACAGTATGAATATGCTTTTAAAGG 1605
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DB 1606 ATAGAACCATTTACATGACAGAGCTTTAGATGTCATGACAGCAAGGCTTTGGGAG 1665
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DB 1666 CTGACAGCTGTCTGGCCATTTCCATGCGCGGACCTGCAAGCTCTAGCCACTGCC 1725
OY 569 HisValGlnArg-----ArgSerArgLeuLysGluProPro 581
DB 1726 CATCAAGATCTCGCTTCTTACCTTTCACAAACGTAACATTCACAAATGCGTCAGAAAC 1785
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DB 1786 TACTACCAAGACTATGATGACAGCTA-----CTCTTACCGGACCTTCCCTTACC 1839
OY 602 HisArgLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyLys 621
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OY 621 HisLeuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTrpGluHisLe 641
DB 1900 CCACAGCAAAATGACACAGAGAGCAAGATCCAGATAGGCCCCACAAACAGTGCATC 1959
OY 641 uCysLysProValProGlnGlu-----SerGluThrGlnTrpIleGln 655
DB 1960 CTGCGCGTG--TTGCCAAGGAGACGATATATCAAGTGTATATGTGACAG 2010
RESULT 7
US-09-864-761-32830
Sequence 32830, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aomico-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO 32830
 LENGTH: 287
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC008249.14
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
 OTHER INFORMATION: EST HUMAN HIT: BR89231.1, EVALUOR 0.00e+00
 OTHER INFORMATION: NT HIT: APL6736.1, EVALUOR 0.00e+00
 OTHER INFORMATION: SWISSPROT HIT: Q02955, EVALUOR 7.00e-03
 US-09-864-761-32830
 Alignment Scores:
 Pred. No.: 1,11e-52 Length: 287
 Score: 531.00 Matches: 95
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 14.47% Indels: 0
 Gaps: 0
 DB: 10
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 3 CGCTGGCATGATGAGGAGCTAGACACCATGAGCAATCCAGTGTGTAAGATGAGCCA 62
 43 AlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHis 62
 63 GCTGCGATCAAGTCCACCTCTTGAACACTTCTTGAATTCACCTACAGCAGCCCAT 122
 63 SerAlaGlyLeuThrLeuIleTrrTyrThrArgGlnAspArgAspLeuGluPro 82
 123 TCGACTGACCTTACTCTGATCTGGATTTGACCTGAGGAGGACCGGACCTTGAGAGCCA 182
 83 IleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrrPheArg 102
 183 ATTACTCTCCGCTCCCGAGAGACCGCATTTAGTAAGAGAGAAAGATGCTGTGTCGCG 242
 103 ProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
 243 CCCACTCTCCCTCAATGACATGCGCAACTATATCTGCACTGATTAAGG 287
 RESULT 8
 US-09-981-421-3
 Sequence 3, Application US/09981421
 Patent No. US20020098185A1
 GENERAL INFORMATION:
 APPLICANT: Sims, John E.
 APPLICANT: Mohler, Kendall M.

APPLICANT: Born, Teresa L.
 TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
 FILE REFERENCE: 3086-A
 CURRENT APPLICATION NUMBER: US/09/981,421
 CURRENT FILING DATE: 2001-10-17
 PRIOR APPLICATION NUMBER: US 60/241,408
 PRIOR FILING DATE: 2000-10-18
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 1626
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1626)
 OTHER INFORMATION:
 US-09-981-421-3
 Alignment Scores:
 Pred. No.: 4.76e-51 Length: 1626
 Score: 528.00 Matches: 174
 Percent Similarity: 46.03% Conservative: 93
 Best Local Similarity: 30.00% Mismatches: 215
 Query Match: 14.39% Indels: 98
 Gaps: 27
 DB: 10
 US-10-061-727-2 (1-687) x US-09-981-421-3 (1-1626)
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 28 CTTTGCGTCTTATATCTCTA-----AGCACTGGAGAAATCT 63
 24 CysAspAspTrrGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
 64 TGT-----ACTTCACGTCCTCCACATCTACTGTGTGTAAGGGAACCT 105
 43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
 106 TTCTATCTGAACCATTTGC-----TCGTTCTCATCTTGA 138
 62 HisSerAlaGlyLeuThrLeu---IleTrrTyrThrArgGlnAspArgAspLeuGlu 80
 139 CATGAGATTGAAACCAACCAACCAAGCTGTGTACAAAGAGTGATCAGAGAACTGTG 198
 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrr 100
 199 GAG---CTGAACCCAGG---ACTTCCTGAGATGCTTTGATGATGTTTGGAG 252
 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
 253 TTTTGCCCACTTACGTTGATGATGACAGGATCTTTTCCAAATGAAATAATTAATTA 312
 121 TyrCysSerLysValAlaPheProLeuGluValIleGln-----LysAspSerCysPhe 138
 313 CAG-----AAATGAAATTAATTAATGATCAGAGAAATTAACACACTGTTTC 360
 139 Asn-----SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154
 361 ACTGAAGACAGACTACTGTAATAATTTGGAATTTAAATAATTTT-----408
 155 IleGlnArgIleThrCysProLeuValAspGlyTyrPheProSerSerValLysProThr 174
 409 ---CAGTTAATCTGTGAANC-----AGTTACATCAAAACAGTGTCAACAGACA 456
 175 IleThrTrrTrrMetGlyCysTrrLysIleGlnAsnPheAsnValIleProGlu---193
 457 ---TCATTGTATGAAGACTTAATAAAGCTACTGAGAGAACATTAATAAACCAACAGATA 513
 194 GlyMetCAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213
 514 AAGAAAGACCGCAGATT-----GAGATCAGGGGTATTACTCTGCGTG 558

QY 214 ValThrTyrProGluAsnGluValGthrPheHISLeuThrArgThrLeuThrValIlyVal 233
DB 559 CATTTCCTTCATCATATGAAACATATTAATCATCAACAAACCTTCATTAACATA 618
QY 234 ValGlySerProIySerAsnAlaValProProValIleHisSerProAsnAspHisValVal 253
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QY 254 TyrGlyGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeu 273
DB 679 GTGGAATTA-----GAAAAAAGCTAAGCTCACTGC-----TCTCTTG 720
QY 274 MetAspSerArgAsnGluValTyrThrIleAspGlyIyIySerProAspAspIleThr 293
DB 721 CTGATGGAAGAGATGATATATGATGTTGGGGAAGAAATGATCGATCTCTAT 780
QY 294 IleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThr 313
DB 781 ATA-----CATGAAAGAAAGAAATGAAATGAAATATATGACT 813
QY 314 -----GlnIleLeuSerIleIyIyValIyValThrSerGluAsp 325
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DB 874 CTAATGTTTATATATATGACATGCTGGCCAGCACGGAGGCAAGACACCAAAAGCTTC 933
QY 346 IyValIyGluIyIy-----ValProAlaProArgTyrThrValGluLeu 360
DB 934 ATCTTGTAAGAAAGACAGACATGCTGATATCCAGGCCAGCTTCACA----- 984
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeu-----ValValIleLeuIleValVal 377
DB 985 ---AGAGAGATGATCATAGCTGTTTATCTTGGTGGCAGAGTGTGCTAAGTCACTGG 1041
QY 378 TyrHisValTyrTyrPleuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu 397
DB 1042 TGTGTCAATTAAGATGATGCTGTTCTATTTATAGACTTAACAGAGAGAGATGAA 1101
QY 398 ThrIleLeuAspGlyIyIySerGluTyrAspIleTyrValSerTyrAlaArg----- 413
DB 1102 ACATTAACAGATGAAACATATGATGCTTGTGTCTTAACCTAAAGAAATGCCGACT 1161
QY 414 ---AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgIyValLeuGluAsnGlu 432
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DB 1222 TTTGGGTATATGATATGATATTTGAAGGAGTGTAGCTGAGAGAGCTGTGTTGAT 1281
QY 453 AlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerProAspTyr 472
DB 1282 GAAATCACTCACTAGTAGAGAAAGCCGAAAGCTATATCTTCTTAATAAAGTTAT 1341
QY 473 ValThrGluIySerIleSerMetLeuGluPheIyIyLeu-----GlyValMetCysGlnAsn 491
DB 1342 ATGCTTAATGAGTCAAGTATGAACTTGAAGAGTCACTCAATGAAGCATTTGGAGAA 1401
QY 492 SerIleAlaThrIyIyLeuIleValValGluTyrArgProLeuGluHisProHis----- 509
DB 1402 AAAAT-----AAATATATCTTAATGAATTAACCTGTATCTGACTTCACATTTCTG 1455
QY 510 ProGlyIleLeuGlnIyIySerGluSerValSerPheValSerTyrPlyGlyIyIySer 529
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QY 530 IyHisIleSerGlySerIyPheTyrPlyValAlaLeuArgLeuAlaLeuProLeuAspSerLeu 549
DB 1516 CTTTCTTATTAACAGAGTTCGAGAAAGACTTCTTACTTAATGCTTCAGAAACAGTC 1575
RESULT 9

US-10-157-447-1
Sequence 1, Application US/10157447
Patent No. US20020143155A1
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2P1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,447
FILING DATE: 28-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/578,178
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/110,618
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hu2P1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1626
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..1623
NAME/KEY: sig_peptide
LOCATION: 1..57
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-157-447-1
Alignment Scores:
Pred. No.: 4.76e-51 Length: 1626
Score: 528.00 Matches: 174
Percent Similarity: 46.03% Conservative: 93
Best Local Similarity: 30.00% Mismatches: 215
Query Match: 14.39% Indels: 98
DB: 12 Gaps: 27
US-10-061-727-2 (1-687) x US-10-157-447-1 (1-1626)
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DB 28 CTTGGGTCTTATATCTGTA-----AGCACTGCAAGATCT 63

QY 24 CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
 DB TGT-----ACTTCAAGTCCCAACATTAAGTGGTTGAAGGGAACCT 105
 QY 43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTrpSerThrAla 61
 DB TTTATCTGAAGAACATTCG-----TCGTGTTCACTTGA 138
 QY 62 HisSerIleGlyLeuThrLeu---IleTrpTrpThrArgGlnAspArgAspLeuGlu 80
 DB CATAGAGTTGAACACCAACCAAGCTGTACAAAGCACTGATACAGGAACATGTG 198
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
 DB 199 GAG---CTGAAGCCCAAG---AGTTCTCGAGAAATGCTTTGCATGATGTGTTTGGAG 252
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpThrCysMetLeuArgAsnThrThr 120
 DB 253 TTTTGGCCAGTTGAGTTGATGACACAGATCTTACTTTCCAAATGMAAAATTAATACT 312
 QY 121 TyrCysSerLysValAlaPheProLeuGluValGln-----LysAspSerCysPhe 138
 DB 313 CAG-----MAATGMAATTAATGTCATCAGAGAAATMAACACAGCTGTTTC 360
 QY 139 Asn-----SerProMetLysLeuProValHisLysLeuTrpIleGluTrpGly 154
 DB 361 ACTGAAGACACAGTAACTAGTAAATTTGTGAAGTTAAATTTT----- 408
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 QY 194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTrpThrCysVal 213
 DB 514 AAGAAAGAACGCCGAGTT-----GAAAGTACAGGGGTATTAATCTCCGCGCTG 558
 QY 214 ValThrTrpProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 233
 DB 559 CATTTCCCTTCATCATTAATGAAGAACTATTATATACCAAAACCTCAATATACAAATA 618
 QY 234 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisValVal 253
 DB 619 GTGGAAGATCCGAGTAATAGTCCGTTCTTGTGACCAAAAGCTTAACCATTTGTCA 678
 QY 254 TyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTrpPheSerPheLeu 273
 DB 679 GTGGAATTA-----GAAAAAAGCTAAGGCTCAACTGC-----TCTCTTTG 720
 QY 274 MetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThr 293
 DB 721 CTGAATGAAGAGATGATATTATTGAGTTGGGAAAGAAATGATCGATCTTAAT 780
 QY 294 IleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThr 313
 DB 781 ATA-----CATGAAGAGAAAGAAATGAGATTAATGACT 813
 QY 314 -----GlnIleLeuSerIleLysLysValThrSerGluAsp 325
 DB 814 CCAGAGGCAAAATGCGATCTTCAAAAGTATGAGATTAATTAATTTGTGTAAGCAAT 873
 QY 326 LeuLysArgSerTrpValCysHisAlaArgSerAlaLysGlyValAlaAlaLysAlaAla 345
 DB 874 CTAAATGTTTATATATATGCACTGTGGCAGCGAGCGACAGACCAAAAGCTTC 933
 QY 346 LysValLysGluLys-----ValProAlaProArgTrpTrpValGluLeu 360
 DB 934 ATCTTGATGAGAAAGACAGACATGCTGATATCCAGCGCAAGCTCTTCA----- 984
 QY 361 AlaCysGlyPheGlyAlaThrValLeuLeu-----ValValIleLeuIleValVal 377

DB 985 ---AGAGGAATGATCATAGCTGTTTGATCTTGGTGGCAGTACTGTCCCTAGAGACTGTG 1041
 QY 378 TyrHisValTrpLeuGluMetValLeuPheTrpArgAlaHisPheGlyThrAspGlu 397
 DB 1042 TGTGTCAATTAATAGATGACTGTGGTTCTATTATTATAGACATTAACGAGAGAGATGAA 1101
 QY 398 ThrIleLeuAspGlyLysGluTrpAspIleTrpValSerTrpAlaArg----- 413
 DB 1102 ACATTAACAGATGAGAAACATATGATGCTTTGTGTCTTAACCTAAAGAAATGCCGACT 1161
 QY 414 ---AsnAlaGluGluGluGluPheValLeuThrLeuArgGlyValLeuGluAsnGlu 432
 DB 1162 GAAATGAGAGAGAGACACCTTTGCTGTGACATTTTCCAGGGGTGTGAGAGAAACAT 1221
 QY 433 PheGlyTrpLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
 DB 1222 TTTGGGTAATAGTTATGCAATTTTGAAGGAGATGATGCTGTGAGAGAGCTGTGTTGAT 1281
 QY 453 AlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerProAspTrp 472
 DB 1282 GAATCCACTCAGTATGAGAAAGCCGAAAGCTAATCATTTGCTTAAGTAAAGTTAT 1341
 QY 473 ValThrGluLysSerIleSerMetLeuGluPheLysLeu---GlyValMetCysGlnAsn 491
 DB 1342 ATGTCTAATGAGCTCAGTATGAACTTGAAGAGTCAATGAAGCATTTGCTGGAAGA 1401
 QY 492 SerIleAlaThrLysLeuIleValAlaGluTrpArgProLeuGluHisProHis----- 509
 DB 1402 AAAAT-----AAATTAATCTTAATTAATTAATTAACCTGTACTGACTTCACATTTCTG 1455
 QY 510 ProGlyIleLeuGluLeuLysGluSerValSerPheValSerTrpLysGlyGluLysSer 529
 DB 1456 CCCCAATCAGCTAAAGCTTTGAATCTCACAGAGTTCTGAAGTGAAGGCGGCAATAAATCT 1515
 QY 530 LysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeu 549
 DB 1516 CTTTCTTAATACGAAAGTTCTGTGAAGAACCTTCTTAATTAATGCTTCCAAAAACAGTC 1575
 RESULT 10
 US-10-011-548-9
 ; Sequence 9, Application US/10011548
 ; Publication No. US2003055218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Timans, Jacqueline C.
 ; Debets, Johannes Eduard Maria
 ; Antonius
 ; Sana, Theodore R.
 ; Bazan, J. Fernando
 ; Kastelein, Robert A.
 ; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
 ; Methods
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/011,548
 ; FILING DATE: 22-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/173,151
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 60/065,776

FILING DATE: 17-NOV-1997
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196
 TELEFAX: (650)496-1200
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2314 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 109..1905
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-10-011-548-9

Alignment Scores:
 Pred. No.: 6.05e-47 Length: 2314
 Score: 495.00 Matches: 181
 Percent Similarity: 44.25% Conservative: 127
 Best Local Similarity: 26.01% Mismatches: 288
 Query Match: 13.49% Indels: 104
 Gaps: 27

US-10-061-727-2 (1-687) x US-10-011-548-9 (1-2314)
 QY 11 TyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArgCysAspAspTyrGlyLeuAsp 30
 Db 128 TATTCTTGGCTTGGTTCAGCA-GAGCAATTAAAGGATTAAATTACAGTTGTTCC 186
 QY 31 ThrMetArgGlnIleGlnValPhe-----GluAspGluProAlaArgIleLysCys 47
 Db 187 ACAAAAAACCTCTTGGACATATTCTCAAGAGTGAAGAGAAATTTGCTTATTTTGT 246
 QY 48 ProLeuPheGlu-----HisPhe----- 53
 Db 247 GATTTACAGGACCAAGAAATCACTTCTGCCACAGAAATGCACTCTACCAAAACAA 306
 QY 54 -----LeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIle 69
 Db 307 GTCCCTGAGACCTGCGCTTCATGGTAAAGCAACCTATCT-----GATGCCAA 357
 QY 70 TrpTyrTrpThrArgGlnAspArgAspLeuGluProIleAsnPheArgLeuProGlu 89
 Db 358 TGGTACCAACAACCTTGGAATGAGATCCATTAGAGACATTAGAAACCTATCTCT--- 414
 QY 90 AsnArgIleSerLysGlnLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109
 Db 415 ---CACATCATTCAGACAAATGATACCTTCACTTTTGAACCCAGGGGTGAATATCT 471
 QY 110 GlyAsnTyrThrCys-----MetLeuArg-----AsnThrThrTyrCysSer 123
 Db 472 GGGTCATATATTGTAGACCAACAAAGATTAAGAGCCCTTATGATAGACCTGTGTGTC 531
 QY 124 LysValAlaPheProLeuGlnValGlnLysAspSerCysPheAsnSerProMetLys 143
 Db 532 AGATGATTTTAAAGTTAAGCCCAAGACAAATGATCTCTGTGATGATTCGCATCA--- 588

QY 144 LeuProValHisLysLeuTyrIleGluTyrGly---IleGlnArgIleThrCysProAsn 162
 Db 589 -----CATAGACAGACCTACTTCTTGGAGACATGCGCTCATATTTCTTCCCAAG 639
 QY 163 ValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly----- 180
 Db 640 CTCAGCTGCCAA---AGTATACACAAAGCTCCAGCGGTACCTGGTACAAAGATGAAAA 696
 QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 Db 697 CTCCTCTCTGTGAAAGAGACCAAGATCGTAGTGAAGTT----- 741
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
 Db 742 -----TATGACTATACACAGGACCATATGATGATGATTAACATCAGTCGATCTG 795
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 Db 796 AGTTCGTGACAGTCAGACGCTGTTGTTCAAGTGAACCACTTGGAGACATTAACCTG 855
 QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGluGlu 260
 Db 856 AAACCAATATTCGATTCGATCCGTGAGAGC-----ACACTGGAAGTGAACCTTGAAG 909
 QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
 Db 910 CTTTAACTATTAACCTGCAAGACAGATTGGCTTTGAAGAGGCTTTAAACCTGTCATA 969
 QY 281 TrpThrThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 Db 970 AATGTGATCATC-----AAAGATTCTGACCTTAAGTGAAGTCTCATGACTGAG 1020
 QY 301 SerIleSer---HisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 319
 Db 1021 GCGAAAAGTATTAAATCATTCATTAAAGATGAATCATTTAGCGTAAATATATCTTGA 1080
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 Db 1081 AAGTCACTCAGCGTGAATCTTCCAGAGAGTTGTTGCTTTCGCAAGACTCCATTGGA 1140
 QY 340 GluValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
 Db 1141 AACCAACACCAAGTCCGTCACAGTGAAGAAAG-----AGAGAGAGTGTCTC 1188
 QY 360 LeuAlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIle-----ValVal 377
 Db 1189 CTGTACATCTCGCTTGGACATCGGAGACCTGTGTGCGCTGTGGCGGAGTCCCTC 1248
 QY 378 TyrHisValTyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu 397
 Db 1249 CTCTACAGGACATGATTAATAATGATGCTGTGCTGACCGACCTACCAAGCAAGATCAG 1308
 QY 398 ThrIleLeuAspGlyLysGlnTyrAspIleTyrValSerTyrAlaArg----- 413
 Db 1309 ACCCTTGGGATTAAGAGATTTGATGCTTGTATCTTAAGCAAAAGACCTCTTTT 1368
 QY 414 -----AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGly 427
 Db 1369 CCNAGTGAAGCCACTTCATCTGTAGTGAAGAACTTGGCCCTGAGCTATTTCTGAT 1428
 QY 428 ValLeuGluAsnGluPheGlyTyrLysLysCysIlePheAspArgAspSerLeuProGly 447
 Db 1429 GTTTTAGAAACAAATATGATGATGCTGTGCTTGAAGAGATGTGGCTCAGGA 1488
 QY 448 GlyAsnThrValGluAlaValPheAspPheIleGlnAspSerArgArgMetIleValVal 467
 Db 1489 GGAAGTATGACAGAGACATTTGTGCAATTATTAAGAGAGCAAGAGAAATTTATTC 1548
 QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
 Db 1549 TTGACCCCACTATGTCAATGAGCAACCACTTTTGAACATCAAGCAAGCATGATCTT 1608
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Db 1609 GCCTTGATGATCA---ACACTGAAATCATTTATTAATTAAGTCTCTTACTTCCAGAG 1665
Qy 504 ProlLeuGlnIleProHisProGlyIleLeuGlnLeuLysGlnSerValSerPheValSer 523
Db 1666 CCAAGACTCTCACTCATCTC---GTGAAAAAGCTCTCAGGGTTTGTGCCACAGTTACT 1722
Qy 524 TPlySGlyGlyLysSerLysHisSerGlySerLysPheThrLysAlaLeuArgLeuAla 543
Db 1723 TGGAGAGGCTTAAATACAGTCTCCCAATTCTAGGTTCTGGCCAAAATCCCTACAC 1782
Qy 544 LeuProLeuArgSerLeuSerAlaSerSerGlyTTPasnGlnSerCysSerSerGlnSer 563
Db 1783 ATGCGCTGTAATAAAC---TCTCAGGAGATTCACTGGAACAGCTCAGAAATTACTAG- 1838
Qy 564 ArgPheSerLeuAspHisValGlnArgArgArgSerArgLeuLysGlnProProGlnLeu 583
Db 1839 GATTTTTCAGTGAAGAGACTCAGTAGAACAGAACCACTGGAGAGGCT-CCACAGCTTA 1897
Qy 584 GlnSerSerGlnArgAlaIleGlySerPro-----ProAlaProGly***MetSerLys 601
Db 1898 AGGAATGCTGAATGAGCCCTGAGAGCCCTCCAGTCCACTCCTGGG---ATAGAGATG 1954
Qy 602 HisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrcysGlnGluAsn 621
Db 1955 TT-GCTGACAGAACTCAGCTCTGTGTGTGTGTCTC----- 1992
Qy 622 HisLeuArgAsnLysSerArgAlaGluIleHisGlnProGlnThrGlnHisLeu 641
Db 1993 AGGCTGATGAAATTCAGAAAGACTCTCTG----- 2022
Qy 642 CysLysProValProGlnGlnSerGlnThrGlnThrIleGlnAsnGly 657
Db 2023 -----CCAGCACCAAGCAAGCTTGATGACAAATGG-----AATGGG 2058

RESULT 11
US-10-212-287-6
; Sequence 6, Application US/10212287
; Publication No. US20030003542A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John
; APPLICANT: Born, Theresa
; TITLE OF INVENTION: ACPL DNA and Polypeptides
; FILE REFERENCE: 2872-US
; CURRENT APPLICATION NUMBER: US/10/212,287
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: PCT/US99/01420
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/072,301
; PRIOR FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 2681
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (484)..(2283)
; OTHER INFORMATION:
US-10-212-287-6

Alignment Scores:
Pred. No.: 7.78e-47 Length: 2681
Score: 495.00 Matches: 181
Percent Similarity: 44.25% Conservative: 127
Best Local Similarity: 26.01% Mismatches: 288
Query Match: 13.49% Indels: 104
DB: 9 Gaps: 27
US-10-061-727-2 (1-687) x US-10-212-287-6 (1-2681)

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Qy 11 TyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArgCysAspAspTrpGlyLeuAsp 30
Db 503 TATTTCTTTGGCTGTGTGTGAAGA-GAGCGAATTTAAAGATTAAATTTCCAGGTGTCC 561
Qy 31 ThrMetArgGlnIleGlnValPhe-----GluAspGlnProAlaArgIleLysCys 47
Db 562 ACAAAAAAATCCTTTGACATATTTCTACAGAGAGTGAAGAGAAATTTCTTATTTCT 621
Qy 48 ProlLeuGln-----HisPhe----- 53
Db 622 GATTTACAGAGCCAGCAAAATCACATTTCTGCCACAGAAATGACTCTACCAAAAACA 681
Qy 54 -----LeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIle 69
Db 682 GTCCCTGAGACACTGCCCTTCAATGGGTATTAAGACTTCT-----GATGTCCA 732
Qy 70 TrpTyrTrpThrArgGlnAspArgAspLeuGlnProIleAsnPheArgLeuProGln 89
Db 733 TGGTACCAACAACCTTCGAATGAGATCCATTAGAGACATTAGAAAGCTATCTCT--- 789
Qy 90 AsnArgIleSerLysGlnLysAspValLeuTyrPheArgProThrLeuLeuAspThr 109
Db 790 ---CACATCATTCAGCAAAATGTACCTTCACTTTTGAACCCAGGGGTGAATTAATCT 846
Qy 110 GlyAsnTyrThrCys-----MetLeuArg-----AsnThrThrTyrcysSer 123
Db 847 GGGTCAATATATTTGTGAGCCCAAGATGATTAAGAGCCCTATGATCTCTGTCTGTC 906
Qy 124 LysValAlaPheProLeuGlnValValGlnLysAspSerCysPheAsnSerProMetLys 143
Db 907 AAGATGATTTTAAGATTAAAGTGAAGCCCAAGAAATGATCTCTGTGAGATTCGGATCA--- 963
Qy 144 LeuProValHisLysLeuTyrIleGlyTyrGly---IleGlnArgIleThrCysProAsn 162
Db 964 -----CATAGCAAGAACCTTACTTCTTGAGAGCACTGCTCTATTTCTTCCCCAGT 1014
Qy 163 ValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly----- 180
Db 1015 CTCAGCTGCCA---AGTAGTCACAAAGTCCAGCGTACCTGTACAGAAATGAAAA 1071
Qy 181 CysTyrLysIleGlnAsnAspAsnValIleProGlnIleMetLysLeuSerPheLeu 200
Db 1072 CTCCTCTGTGTGAAGAGCAACGAAATCGTAGTGAGAGTT----- 1116
Qy 201 IleAlaLeuLysSerAsnGlnLysenTyrThrCysValAlaThrTyrcysGlnAsnGly 220
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Qy 221 ArgThrPheHisLeuThrArgThrIleLeuThrValValGlySerProLysAsnAla 240
Db 1171 AGTTGCGAGCACTCAGACTGTTGTTCAGGTAGAACCAATGTGGAGACATAAATCTC 1230
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGlyLysGlnProGlyGln 260
Db 1231 AAACGATATTTCTGATCTGTGAGAGC-----ACACTGAAATAGAACTTGAAAG 1284
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Qy 301 SerIleSer---HisSerArgThrGlnAspGlnThrArgThrGlnIleLeuSerIleLys 319
Db 1396 GCGAAAGATTTAAATCACTTAAGATGAATGATGAGGTATATATCACTTTGGA 1455
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Oy 340 GtUvAlAlAtySvAlAlAtySvAlTySvAlGtUvAlProAlProkGtYrThrValGlu 359
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Oy 360 LeuAlAcysGtYrPheGtYrAlAtHrValLeuValValAlleuAlle-----ValVal 377
Db 1564 CTGTAACATCCGCTTGGAACAATCCGGAGACCTGTGTGGCGGTGGCGGAGTGCCTC 1622
Oy 378 TyrHtSvAlYrTrPLeuGluMetValLeuPheYrAlAlAhIspHeGtYrThrsPglu 397
Db 1624 CTCTACAGGCACTGATTTGAAATAGTGTCTGTCTACCCGACCTACACAGCAAGATCG 1683
Oy 398 ThrIleuAspGtYrGtYrAspAlleTyValSerTyAlArG----- 413
Db 1684 AGCGCTGGGATTAAGAAAGATTTGATGTCTTGATCTCATGCAAAATGGAGCTCTTTT 1743
Oy 414 -----AsnAlaGluGluGluGluPheValLeuPheThrLeuArgly 427
Db 1744 CCAAGTAGGCGCACTTCACTCTGAGTGAAGAAACACTTGCGCTTAGCCTATTTCTGAT 1807
Oy 428 ValLeuGluAsnGluPheGtYrYrTySLeCysAlIephAspArgSerLeuProGly 447
Db 1804 GTTTTAAAGAAACAATATGTGATATAGCTGTGTGTGGTGAAGAGATGTGCTCAGGA 1863
Oy 448 GlyAsnThrValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValVal 467
Db 1864 GGAGGTGATGCAAGCAATGTGTGAGCATTTATTAAGAGAAAGCAAGAAAGAAATTTATTC 1923
Oy 468 LeuSerProAspYrValThrGluYrSerIleSerMetLeuGluPheYsLeuGlyAl 487
Db 1924 TTGAGCCCCCAATATGTCAATGGAACCCAGTATCTTGAACCTACAGCAGAGATGATCTT 1983
Oy 488 MetCysGlnAsnSerIleAlaThrTySLeuIleValValGluTyR-----Arg 503
Db 1984 GCGTTGATGATCA-----ACACTGAACATCATTTATTAATGTTCTGTTACTTCCAGAG 2046
Oy 504 ProLeuGluHtIspRhtSproGtYrIleLeuGluMetYsGluSerValSerPheValSer 523
Db 2041 CCAGAGTCTCACTCACTCACTTC--GTGAAAGAAAGCTCTCAGGGTTCGCCACAGTACT 2097
Oy 524 TrpYsGtYrGluYrSerGtYrHtSserGtYrSerTySLePheTrpYsAlleuPheLeuAl 543
Db 2098 TGGAGAGGCTTAATAATCATGTTCTCCCAATTCATAGGTTCTGGGCCAAATAGGCTACAC 2155
Oy 544 LeuProLeuArgSerLeuSerAlaSerSerGtYrTrpAsnGluSerCysSerSerGlnSer 563
Db 2158 ATGCGTGTGAANAAC---TTCAGAGGATTCACGTGAAACACAGCTCAGATTATCCTGAG 2213
Oy 564 AspIleSerLeuAspHtSvAlGlnArgArgArgSerArgLeuYsGluProGluLeu 583
Db 2214 GATTTTTCAGTGAAGAAAGACCTCAGTGAAGAACAGAAACACCTGGAGAGAGCT-CCAGAGCTA 2272
Oy 584 GlnSerSerGluAlaAlaIleGtYrPro-----ProAlaProGly**MetSerTyS 601
Db 2273 AGGAATGCTGAATGAGCCCTGAGAGCCCTCCAGTCTCAGTCCCTGGG--ATAAGATG 2329
Oy 602 HisArgGtYrSerSerAlaThrCysArgCysCysValThrTyTCysGluGluGluAsn 621
Db 2330 TT-GCTGGACAGAACTCAGACGCTGTGTGTGTGTGTC----- 2367
Oy 622 HisLeuArgAsnTySserArgAlaGluIleHisAsnGlnProGluIleTrpGluThrHisLeu 641
Db 2368 AGGCTGATGAGAAATTCAAAAGAGTCTCTG----- 2397
Oy 642 CysTySProValProGlnGluSerGluThrGlnTrpIleGlnAsnGly 657
Db 2398 -----CCAGCAACCAAGCAAGCTTGATGAGCAATAG-----AATGGG 2433

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      : APPLICANT: Mohler, John E.
      : APPLICANT: Born, Teresa L.
      : TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS.
      : FILE REFERENCE: 3086-A
      : CURRENT APPLICATION NUMBER: US/09/981,421
      : CURRENT FILING DATE: 2001-10-17
      : PRIOR APPLICATION NUMBER: US 60/241,408
      : PRIORITY FILING DATE: 2000-10-18
      : NUMBER OF SEQ ID NOS: 5
      : SOFTWARE: PatentIn version 3.1
      : SEQ ID NO 1
      : LENGTH: 2681
      : TYPE: DNA
      : ORGANISM: Homo sapiens
      : FEATURE:
      : NAME/KEY: CDS
      : LOCATION: (484)..(2283)
      : OTHER INFORMATION:
      : US-09-981-421-1

Alignment Scores:
Pred. No.:          7,78e-47           Length:         2681
Score:             495.00              Matches:         181
Percent Similarity: 44.25%              Conservative:    127
Best Local Similarity: 26.01%            Mismatches:     288
Query Match:       13.49%               Indels:         104
DB:                10                   Gaps:           27

US-10-061-727-2 (1-687) x US-09-981-421-1 (1-2681)

QY   11 TyrPheTyrgIyIleLeugInSerAspAlaISerGluArgCysAspAspTrpGlyLeuAap 30
Db   503 TATTTCTTGGCTGTGTTGCAGGA  GACGCAATTAAAGATTATTAATTCAGTGTC 561
QY   31 ThrMetArgInIleGlnValPhe-----GluSpGlnProAlaArgIelysCys 47
Db   562 ACAAAAAAACCCCTTGGACATAITTCACAAGAGTGAGAGAATTGCTTATTTGT 621
QY   48 ProLeuPheGlu-----HisPhe----- 53
Db   622 GATTTCACAGGCCACAGAAATCACATTTCTGCCACAGAAATGACTCTCACAAAACA 681
QY   54 -----LeuLysPheAsnTYrSerThrAlaHisSerAlaGlyLeuThreule 69
Db   682 GTCCCTGAGACCTGCCCTTCATCGGTAGTAGACACTATCT-----GATGCCAA 732
QY   70 TrpTYrTrpThrArgGlnAspArgAspleuGlnGluProIlleasnPheArgLeuProGlu 89
Db   733 TGGTACCAACAACCCTGCAATGTGAGATCATCTTAGAGACATTAGAAAGACTATCT--- 789
QY   90 AsnArgIleSerIysGluLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109
Db   790 ---CACATCATTCAGGACAAATGATGACCTTCACCTTTTGAACCCACAGGGGAAATATCT 846
QY   110 GlyAsnTYrThrCys-----MetLeuArg-----AsnThrThyTYrCysSer 123
Db   847 GGCGTCATATATTATTAGAACCCAGATGATTAAGAGCCCCCATGATGAGACCTGTGTGTC 906
QY   124 LysValAlaPheProLeuGlnValValGlnLysAspSerCysPheAsnSerProMetLys 143
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QY   144 LeuProValHisLysLeuTYrIleGluTYrGly---IlleGlnArgIlleThrCysProAsn 162
Db   964 -----CATTAAGCAAAGACTATCTTTGGAGACCTGGCGCTCATATTTCTAGCCCCAGT 101
QY   163 ValAspGlyTYrPheProSerSerValLysProThrIlleThrTrpTYrMetGly----- 180
Db   1015 CTCAGCTGCCAA---AATTGATGCAACAAGTCCAGCGGTATACCTGTGTACCAAGATGAGAAA 1077
QY   181 CysTYrLysIlleGlnAsnPheAsnAsnValIlleProGlnGlyMetAsnLeuSerPheLeu 200

```


GenCore version 5.1.4 ps 4578
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 30, 2003, 09:52:34 ; Search time 1672 Seconds

(without alignments)
6654.485 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669
Sequence: 1 MTLWCVSVLYFYGILGSDA.....SALALHHFTLSDNNDFYLL 687

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_plus.p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US10061727/runat_23042003_083116_7900/app_query.fasta_1.839
-DB=EST -QFMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10061727@cgn2_1.1456@runat_23042003_083116_7900 -NCRU=6 -TCPU=3
-NO XLPXY -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estrov.*
6: em_estcpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_ggs.*
18: em_ggs_hum.*
19: em_ggs_inv.*
20: em_ggs_pin.*
21: em_ggs_vrt.*
22: em_ggs_fun.*
23: em_ggs_mam.*
24: em_ggs_mus.*
25: em_ggs_other.*
26: em_ggs_pro.*
27: em_ggs_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1865	50.8	1549	11 BC016141	BC016141 Homo sapi
2	1289	35.9	849	9 AL543511	AL543511 AL543511
3	1281	34.9	873	13 B1862501	B1862501 603390624
4	1277	34.8	880	13 B1330085	B1330085 602982187
5	1124	30.6	814	14 B0006059	B0006059 UI-H-E11-
6	1012	27.6	723	10 AW211290	AW211290 uc079b07.y
7	999	27.2	756	9 A1303998	A1303998 uc63d12.y
8	989	27.0	888	13 B1331848	B1331848 602982528
9	927	25.3	910	12 BE892231	BE892231 601435065
10	915	24.9	580	13 B1346913	B1346913 376288 MA
11	900	24.5	596	10 AV656295	AV656295 AV656295
12	876	23.9	489	14 BM760155	BM760155 K-EST0040
13	873.5	23.8	598	9 AA237107	AA237107 mw96b02.x
14	863	23.5	789	10 AV659167	AV659167 AV659167
15	858	23.4	652	10 BB625831	BB625831 BB625831
16	853	23.2	533	9 AA239486	AA239486 mw98g02.x
17	834	22.7	643	10 BB626271	BB626271 BB626271
18	834	22.7	676	10 BB653335	BB653335 BB653335
19	817	22.3	643	9 AA107505	AA107505 mp05d08.x
20	807.5	22.0	885	12 BF237012	BF237012 602026645
21	805	21.9	646	10 BB612046	BB612046 BB612046
22	784	21.4	923	9 AL544533	AL544533 AL544533
23	769	21.0	500	9 AA571281	AA571281 V190903.x
24	766	20.9	616	10 AV661936	AV661936 AV661936
25	766	20.9	637	10 BB623025	BB623025 BB623025
26	700	19.1	475	14 B0561650	B0561650 HA071P02-
27	687	18.7	545	10 BB63613	BB63613 BB63613
28	685.5	18.7	632	13 B1065068	B1065068 p9f.in.pk0
29	685	18.7	644	9 AA819412	AA819412 UI-R-A0-b
30	675	18.4	537	13 B1340158	B1340158 365346 MA
31	656	17.9	396	14 T08277	T08277 EST06168.in
32	625	17.0	567	14 BM751599	BM751599 K-EST0027
33	602.5	16.4	586	12 BG711109	BG711109 p9f.in.pk0
34	587	16.0	355	10 AV654169	AV654169 AV654169
35	570.5	15.5	938	12 BG032519	BG032519 602301430
36	569	15.5	850	13 B1872969	B1872969 603398140
37	536	14.6	392	10 AA427989	AA427989 64724 MAR
38	497.5	13.6	426	14 T70863	T70863 yd15f12.r1
39	497.5	13.6	570	14 H80590	H80590 yu76e04.r1
40	494.5	13.5	560	13 B1065233	B1065233 p9f.in.pk0
41	488.5	13.3	712	13 B1106737	B1106737 602891267
42	471	12.8	520	9 A1529899	A1529899 ui89g06.y
43	466	12.7	415	10 BB644209	BB644209 BB644209
44	426	11.6	305	10 AA485290	AA485290 64805 MAR
45	394.5	10.8	309	14 T85756	T85756 yd60e03.r1

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
BC016141	BC016141	Homo sapiens, interleukin 1 receptor accessory protein, clone IMAGE:3920152, mRNA.	BC016141	BC016141.1	GI:16359373	Homo sapiens.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Strausberg, R.	Direct Submission
1549 bp	mRNA	linear	HTC 24-OCT-2001							

JOURNAL

Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCPD/DRP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Scott, Michel Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
Series: IRAC Plate: 15 Row: 1 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4504660
This clone has the following problem: frame shifted.

FEATURES

source

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1.1549
/organism="Homo sapiens"
/db_xref="locusid:3556"
/db_xref="taxon:9606"
/clone="IMAGE:3920152"
/rissue_type="Skin, melanotic melanoma."
/clone_lib="NIH MGC_72"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"
BASE COUNT      480 a      340 c      331 g      398 t
ORIGIN
```

Alignment Scores:

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Pred. No.:      1 05e-187      length:      1549
Score:          1865.00      Matches:      349
Percent Similarity: 99.71%      Conservative: 0
Best Local Similarity: 99.71%      Mismatches: 1
Query Match:      50.83%      Indels:      1
DB:              11          Gaps:      0
```

```
nc-10-061-727-2 (1-687) x BC016141 (1-1549)
```

```
1 MetThrLeuLeuTrpCysValValSerLeuLeuTrpGlyGlyLeuGlnSerAspAla 20
|||||
206 ATGACACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 265
|||||
21 SerGluArgCysAspAspTrpGlyLeuAspPheMetArgGlnIleGlnValPheGluAsp 40
|||||
266 TCAAGACGCTGCGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGG 325
|||||
41 GlnProAlaArgGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
|||||
326 GAGCAGCTGCGACATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 385
|||||
42 AlaHisSerAlaGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
|||||
386 GCCCATTCAGCTGCGCTTACTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 445
|||||
43 GlnProIleAsnPheArgLeuProGluAsnArgIleSerIleGlyValAspValLeuTrp 100
|||||
446 GAGCAATTAATCTTCCTCCCGAGAAACGCAATGTAGTAAAGGAGAAAGATGTCTGTGG 505
|||||
45 PheArgProThrLeuLeuAsnAspThrGlyValAsnIleTrpCysMetLeuArgAsnThrThr 120
|||||
```

```
Db 506 TTCGGGCCCACTCTCTCAATGACACTGCGCACTATACCTGATGTAAAGAACTACA 565
|||
Qy 121 TyrCysSerIleValAlaPheProLeuGlnValValGlnIleYasPserCysPheAsnSer 140
|||||
Db 566 TATTGACGCAAAAGTGTGATTTCCCTTGGAAGTGTGTCAAAAAGACACTGTTCATATTC 625
|||||
Qy 141 ProMetIleLeuProValHisIleYleuTrpIleGluTrpGlyIleGlnArgIleThrCys 160
|||||
Db 626 CCATGAAATCTCCAGTGCATTAATCTATATGAAATATGATGATTCAGAGATCACTGT 685
|||||
Qy 161 ProAsnValAspGlyIleTrpPheProSerSerValIleProThrIleThrTrpIleMetGly 180
|||||
Db 686 CCAATGTATGATGATATTTTCTTCCAGTCAAAACGCACTATACCTGTGTATATGAGGC 745
|||||
Qy 181 CysTrpIleIleGlnAsnPheAsnAsnValIleProGluIleMetAsnLeuSerPheLeu 200
|||||
Db 746 TGTATTAATAATACGAATTTTAATGAATATACCCAGAGTATGAACCTGAGTTCTTC 805
|||||
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnIleTrpCysValValThrTrpProGluAsnGly 220
|||||
Db 806 ATGACCTTAATTCATTAATTAATGAATTAATCAATGTGTGTACATATCCAGAAATGGA 865
|||||
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValIleValValGlySerProIleAsnAla 240
|||||
Db 866 CGTACGTTTCATCTCACAGAGCTGCTGTAAGGTATGAGCTCTCCAAAAAATGCA 925
|||||
Qy 241 ValProProValIleHisSerProAsnAspHisValValIleGluIleGluProGlyGlu 260
|||||
Db 926 GTGCCCTCTGTGATCCATTCATCAATCAATGATCATGTGTGTATGAGAAAGAACGAGAG 985
|||||
Qy 261 GlnLeuLeuIleProCysTrpValIleTrpPheSerPheLeuMetLysSerArgAsnGluVal 280
|||||
Db 986 GAGTACTCATCTCCCTGTAGGCTATTTAATGTTCTGATGAGATCTCGCAATGAGGTT 1045
|||||
Qy 281 TrpTrpThrIleAspGlyIleYleYsProAspAspIleThrIleAspValThrIleAsnGlu 300
|||||
Db 1046 TGTGACCATTTGATGTGAAAAAACCGATGATGATCATCTATATGATGATCAATTAAGCA 1105
|||||
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleYleYs 320
|||||
Db 1106 GT-ATAGTCATGTAGTAAAGAGAAAGATGAACAAAGCTGATTTTGACATCAAGAAA 1164
|||||
Qy 321 ValThrSerGluAspLeuLeuYasPserTrpValCysHisAlaArgSerAlaYsGluGlu 340
|||||
Db 1165 GTTACCTCTGAGATCTCAAGCGCAGCTATGTCTGTATGTGTGAAATGCGCAAGGCGAA 1224
|||||
Qy 341 ValAlaIleYsAlaIleYsValIleYsGlnIleYs 350
|||||
Db 1225 GTTCCCAAGCAGCCCAAGGTGAAGCAAAA 1254
|||||
```

RESULT 2

AL543511

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITL

JOURNAL

COMMENT

FEATURES

source

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.
Location/Qualifiers
1. 849
/organism="Homo sapiens"

/db xref="taxon:9606"
 /clone="CSOD1003YK15"
 /clone_lib="LRI.NFL006.PL2"
 /tissue_type="Placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"

BASE COUNT 232 a 206 c 185 g 224 t 2 others
 ORIGIN

Alignment Scores:

d. No.:	1.23e-126	Length:	849
Score:	1289.00	Matches:	238
Percent Similarity:	97.17%	Conservative:	2
Best Local Similarity:	96.36%	Mismatches:	6
Query Match:	35.13%	Indels:	1
DB:	9	Gaps:	0

US-10-061-727-2 (1-687) x AL543511 (1-849)

```

Oy 1 MetThrLeuLeuTrpCysValValSerLeuTrpPheTrpGlyIleLeuGlnSerAspAla 20
Db 110 ARGACACCTCTGTGTGTAGTGTAGTGTCTCTCTTTATAGAACTCTGCAGAAAGTGTATGCC 169
Oy 21 SerGluArgCysAspAspTrpGlyLeuAspTrpMetArgGlnIleGlnValPheGluAsp 40
Db 170 TGAAGACGCTGGAGTACGAGGAGTACGACATAGGACGAAATCCAGAGTTTGAAAGT 229
Oy 41 GluProAlaArgIleCysProLeuPheGluHisPheLeuLysPheAsnTrpSerThr 60
Db 230 GAGCCAGCTCGCATCAAGGCCACCTTTGAACATTTTGAAATTCATCAACAGCAC 289
Oy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTrpTrpArgGlnAspArgAspLeuGlu 80
Db 290 GCCCATTCAGTGGCTTACTGACTGCTGTAATGAGTACGAGACGCGGACCTTGAG 349
Oy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLeuGluLysAspValLeuTrp 100
Db 350 GAGCCAAATTAACCTCCGCTCCCGGAGAACCGATTAAGTAAAGAAATGTGCTGTGG 409
Oy 101 PheArgProThrLeuLeuAsnAspTrpGlyAsnTrpThrCysMetLeuArgAsnThrTrp 120
Db 410 TTCGGGCCCACTCTCTCTCAATGACACTGGCACTATACCTGCAATGTAAAGAACTACA 469
Oy 121 TrpCysSerLeuValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
Db 470 TATTGACAGCAAGTTCAATTCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTC 529
Oy 141 PrometLysLeuProValHisLysLeuTrpIleGluTrpGlyIleGlnArgIleThrCys 160
Db 530 CCCATGAAACTCCCACTGATAAACGTATATAGAAATATGCACTTGAAGGATCACTTGT 589
Oy 161 ProAsnValAspGlyTrpPheProSerSerValLysProThrIleThrTrpTrpMetGly 180
Db 590 CCAATGTATGATGATATTTCTTCTCAAGTCAAAAACACATTCACCTTGATATGGGC 649
Oy 181 CysTrpLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 650 TGTATTAATAATACAGATATTTTATATATGTAATGCCGAGATGATGAAGTATCCCTC 709
Oy 201 IleAlaLeuIleSerAsnGlnGlyAsnTrpThrCysValValThrTrpProGluAsnGly 220
Db 710 ATTCCTTAATTAATTAATGAAATTAACATGTGTTTACATATCCAGAAATATGGA 769
Oy 221 ArgThrPheHisLeuThrArgThrLeuTrpValValGlySerProLysAsn-Al 240

```

Db 770 CGTACGTTTCATTCACACGACTCTACTGTAAAGGTATGAGCTCTCCAAAATATGCAG 829
 Oy 240 aValProPheValIleHis 246
 Db 830 TCCCTCTGTATCATTCAC 848

RESULT 3
 Bi662501
 LOCUS 603390624P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399668 5',
 DEFINITION mRNA sequence.

ACCESSION Bi662501
 VERSION Bi662501.1 GI:16003248
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 873)
 NIH-MGC http://mhc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 Plate: LRAM12018 row: P column: 05
 High quality sequence stop: 838.
 Location/Qualifiers

FEATURES

source
 1..873
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5399668"
 /clone_lib="NIH_MGC_87"
 /tissue_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally, oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

BASE COUNT 272 a 176 c 191 g 234 t

ORIGIN

Alignment Scores:
 Pred. No.: 9.31e-126 Length: 873
 Score: 1281.00 Matches: 257
 Percent Similarity: 96.99% Conservative: 1
 Best Local Similarity: 96.62% Mismatches: 2
 Query Match: 34.91% Indels: 7
 DB: 13 Gaps: 0

US-10-061-727-2 (1-687) x Bi662501 (1-873)

```

Oy 91 ArgIleSerLeuGluLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThrGly 110
Db 1 CGCATTAATGAGGAAATATGCTGTGTGTCGGCCCACTCTCTCATATGACATGGC 60
Oy 111 AsnTrpThrCysMetLeuArgAsnThrTrpTrpCysSerLeuValAlaPheProLeuGlu 130
Db 61 AACTATACCTGCATGTAAAGAACTACTATATGACAGCAAGTTGCAATTCCTTGGA 120
Oy 131 ValValGlnLysAspSerCysPheAsnSerPrometLysLeuProValHisLysLeuTrp 150
Db 121 GT-GTTCAAAAAGACAGCTGTTCAATTCCTCCATGAACTCCCATGATTAACGTAT 179
Oy 151 IleGluTrpGlyIleGlnArgIleThrCysProAsnValAspGlyTrpPheProSerSer 170

```

Db 180 ATGATATGCAATTCAGAGATCACTTGCCAAATGATGATATTTCTCCAGT 239

Qy 171 VALLVSPROTHRIETHTPTPTMETGLYCYSTYLYSILEGIMASNPHESNANVAL 190

Db 240 GTCAACCCGACATATCACTTGATATGAGCGCTGTATTAATAATACAGAAATTTATATATGTA 299

Qy 191 ILEPFGUGLIMETASNLEUSERPHELEULIETALILEULIESTERNANGLIYASNTYR 210

Db 300 ATACCCGAAGGATATGAATGAGTTCATTCATTCCTTAATTTCAATATATGAAATTTAC 359

Qy 211 ThrCysValIValThrTyrProGluSengIYArgThrPheHisIleuThrArgThrLeuThr 230

Db 360 ACATGTGTGTATACATATCCAGAAATGACGACGTTTCATCTCCAGGACTGACT 419

Qy 221 VALLVSVAILGLYSERPROLYSASNAIYALPROCVAILLEHISERPROASNAEP 250

Db 420 GTAAAGTAGTAGGCTCTCAAAAATGCAAGGCCCTGTGATCCATTCACCTATGAT 479

Qy 251 HISVALVALTYRGLULYSGIUPROGLIYGLULILEULILEULIESTERNANGLIYASNTYR 270

Db 480 CATGTGCTATGAGAAACCAAGAGAGAGCTACTCATTCCTGTACGGCTATATTT 539

Qy 271 SerPheLeuMetAspSerArgSengIValTPTPTThrIleAspGlyLYSLSYSPROASP 290

Db 540 AGTTTCTGATGATGATTCGCAATGAGGTTTGATGACCATTCATGATGAAAAAACCCTGAT 599

Qy 291 AspiIethrIle-AspValThrIleSngIuSerIleSerHisSerArgThrIuAspGly 310

Db 600 GACATCATATGTGATGATGATTCACCATTAACGAAATATATGATATGATGAAACGATGAT 659

Qy 310 V-THARGTHRGILNILEUSERILEYS-LYSVALITHTSERGIUASPLEULYARGSE 329

Db 660 AAACAGAACTCAGATTTTGTAGCATCAAGAAAGTTACTCTGAGAGATCTCAAGGGCAG 719

Qy 329 TYRVALCYSHISALYARG-SERIALYSGIYGLULVAL-ALALYSVALIYALYSVALYS 348

Db 720 CTATGTCTGTCTGCTAGAGGGGTCCAAAGGCGAATTTGCCAAAGCAGCAAGGTGAAG 779

Qy 349 GlnLys 350

Db 780 CAGAAA 785

RESULT 4

BI330085 880 bp mRNA linear EST 30-JUL-2001

LOCUS 602982187P1 NCI_CGAP_L1.9 Mus musculus cDNA clone IMAGE:5135061 5',

DEFINITION mRNA sequence.

BI330085

ACCESSION BI330085.1 GI:15014755

VERSION

KEYWORDS EST.

ORIGIN

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 880)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMLT)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LMLT at:

http://image.lml.gov

Place: LMLM1331 row: n column: 22

High quality sequence start: 3

High quality sequence stop: 870.

Location/Qualifiers

1..880

source

FEATURES

source

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5135061"

/clone_id="NCI_CGAP_L1.9"

/lab_host="DH10B (TI phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library."

BASE COUNT 249 a 215 c 193 g 223 t

ORIGIN

Alignment Scores:

Pred. No.: 2,53e-125 Length: 880

Score: 1277.00 Matches: 242

Percent Similarity: 91.22% Conservative: 28

Best Local Similarity: 81.76% Mismatches: 23

Query Match: 34.81% Indels: 6

DB: 13 Gaps: 0

US-10-061-727-2 (1-667) x BI330085 (1-880)

Qy 46 LysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHisSerAlaGly 65

Db 1 CAGTCCCCCTCTTTGAAACACTTCTCGAAGTACACTACAGACATGCCCCATTCCTGCGC 60

Qy 66 LeuThrLeuIleTPTPTTPTThrArgGlnAspArgAspLeuGluProIleAsnPhe 85

Db 61 CTACCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

Qy 86 ArgLeuProGluAsnArgIleSerIleGlnLysAspValLeuThrPheArgProThrLeu 105

Db 121 CGCTCCCAAGAAATCGCATCACTGAGGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

Qy 106 LeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSerLysVal 125

Db 181 CTCATGACACCGGCAATTAACCTGCATGTGAGGAAACACACTTAATGCGACCAAGTT 240

Qy 126 AlaPheProLeuGluValIleGlnLysAspSerCysPheAsnSerProMetLysLeuPro 145

Db 241 GCATTTCCCTGGAAGTGTTCAGAAAGACAGCTGTTCATTCGACATGAGATTCACA 300

Qy 146 ValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCysProAsnValAspGly 165

Db 301 GTGCAAGATGATATATGAACATGCGCATTAATGATCAATGATGATGATGATGATGATGAT 360

Qy 166 TyrPheProSerSerValLysProThrIleThrTyrTyrMetGlyCysTyrLysIleGln 185

Db 361 TACTTCTCTTCCAGTGTCAACCAACGATCGGTCACTTGATTAAGGGTGTACGAATATG 420

Qy 186 AsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeuIleAlaLeuIleSer 205

Db 421 GACTTTCATTAATGATACACCGAGGGCATGAACCTTTTTCATCTCCCTGCTTCA 480

Qy 206 AsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGlyArgThrPheHisLeu 225

Db 481 AATAACGAAATATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

Qy 226 ThrArgThrLeuThrValLysValValIleGlySerProLysAsnAlaValProProValIle 245

Db 541 ACCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599

Qy 246 HisSerProAsnAspHisValValTyrGluLysGluProGlyGluGluLeuLeuIlePro 265

Db 600 TATTTCCAAATGACCGCTGTGTATAGAAAGAACACAGAGAGGAACTGTTATTTCC 659

Qy 266 CysThrValTyrPheSerPheLeuMetAspSerArgSengIValTPTPTThrIleAsp 285

Db 660 TGCAAAGCTATTTATGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 719

Qy 286 GlyLysLysProAspAspIleThrIleAsp-ValThrIleAsnGluSerIleSerHisSe 305

Db 720 GGAAGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779

found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html

MGI:1029177
 Seq primer: -40RP from Gibco
 High quality sequence stop: 427

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/organism="Mus musculus"
/strain="129, C57BL/6J, FVB/N"
/db_xref="taxon:10090"
/clone="IMAGC:2648725"
/clone_lib="NCI CGAP Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI;
Site: 2: NciI; Cloned unidirectionally. Primer: Oligo dt.
Providing samples: Lothar Hennigsausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
32, 37-43 (1999)."
```

THE COUNT	206 a	148 c	182 g	186 t	1 others
PERCENT					

Alignment Scores:

Freq. NO.:	3.67e-97	Length:	723
Score:	1012.00	Matches:	195
Percent Similarity:	89.21%	Conservative:	20
Best Local Similarity:	80.91%	Mismatches:	25
Query Match:	27.58%	Indels:	2
DB:	10	Gaps:	0

US-10-061-727-2 (1-687) x AW211290 (1-723)

QY	209	AspYrThrCysValIvalThrTyrProGluSngIylarGthrPheHisleuthrArygthr	222
Db	2	AAITACACATGATGAGGTACATATCTCGAAGAAACGACACTCTCTTCACTCCACACAGACT	61
QY	229	LeuThrValIlysValIvalGlySerProIysAsnAlaValProProValIleHisSerPro	246
Db	62	GTGACGTGAAGGCGTGCGGCTCACCAAGATGATTCACACCCACAGATCTATTCTCA	127
QY	249	AsnAspHisValValIlyrGluLysGluProGlyGluGluLeuLeuIleProCysThrVal	266
Db	122	AATGACCGGTGTGTCTATGAGAAAGAAACACGAGACGACTGTATTATCTCGAAGATC	181
QY	269	TyrPheSerPheLeuMetAspSerSerArgAsnGluValTrpTrpThrIleAspGlyLys	288
Db	182	TATTTCAGTTCATTATGAGACTCCCAACATGAGGTCTGGTGACCATTTAGTGAAGAG	241
QY	289	ProAspAspIleThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGlu	308
Db	242	CCGATATACGTCACAGTCGACATCATTAATGAAGGTGAATGTATCTTCACAGGAA	301
QY	309	AspGluThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeuLysArg	328
Db	302	GATGAAACAAAGGACTCGAATTTTGAGCATCAAGAAAGCCACCCCGAGGATCTTCANCGC	361
QY	329	SerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAlaLysValLys	348
Db	362	AACATATCTGTATGCTCGAAATACCAAAAGGGAACTGACGAGCTGCCAAGGAGAA	421
QY	349	GluLysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAlaThrVal	368
Db	422	CAGAAAGTCATACCACCAAGATCACAGTGAAGTGGCTGTATATGAGACACAGCT	481
QY	369	LeuLeuValIleValIleLeuIleValValIlyrHisValIlyrTrpLeuGluMetValLeuPhe	388
Db	482	TTTCTGTATGTGTCTTCATTTGTGTGTTCACATGTTTACATGCTCGAGATAGTCTCTTT	541
QY	389	TyrArgAlaHisPheGlyThrAspGluThrIleLeuAspGlyLysGluLysTyrAspIleTyr	408

Db	542	TACGAGCTCATTGTGGAAACGATATGACAATTCTTGTATGAAGAAGACTATGATATTAT	601
Oy	409	ValSerTYRAIArgAlaIleGlnGluGluGluPheValIleLeuLeuThr-IleuArgGlyVa	428
Db	602	GTAAGCTATTGCACACATGTGTGAMAGAGATTTTGCGTCGATACCCCTGCCGTGAAGT	661
Oy	428	IleuGIubAnsngIupheGlyTYRYSLeuCYsIIePheAspArgAspSerLeuProGIYGI	448
Db	662	CATGAGAGATGAGTTTGGATCCCAAGCTGGC-ATCTTCAGACAGATACCAGCTGCTCCGAGG	720
Oy	448	Y 448	
Db	721	A 721	
RESULT 7			
LOCUS	A1303998		
DEFINITION	A1303998	756 bp	mRNA linear EST 08-DEC-1998
	u63d12.y1 Sugano mouse liver mla Mus musculus CDNA clone		
	IMAGE:1867095 5' similar to gb:X85999 M.musculus mRNA for		
	interleukin 1 receptor accessory (MOUSE);, mRNA sequence.		
ACCESSION	A1303998		
VERSION	A1303998.1	GI:3987748	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 756)		
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubnue,T., Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Teisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
TITLE	The WashU-HIMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project		

BASE COUNT ORIGIN	199 a	185 c	167 g	195 t	10 others
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Alignment Scores:
 Pred. No.: 9,78e-96 Length: 756
 Score: 999.00 Matches: 194
 Percent Similarity: 83.86% Conservative: 19
 Best Local Similarity: 76.38% Mismatches: 35
 Query Match: 27.23% Indels: 7
 DB: 9 Gaps: 3

US-10-061-727-2 (1-687) x A1303998 (1-756)

QY 7 ValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArgCysAspAsp 26
 Db 3 TTSATGAGTCCTCTTCTATGAGATCTGCAAGATCATCTTCGAGCGCTGTGATGAC 62
 QY 27 TrrGlyLeuAspThrMetCArgGlnIleGlnValPheGluAspGluProAlaArgIleLys 46
 Db 63 TGGGAGCTAGATACATGCAATCCAAATCCAGTTCCTTGAATGAGCGGCTCCAAATCAAG 122
 QY 47 CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeu 66
 Db 123 TGGCCCTCTTGAACACTTCTGAGATGACATGACAGACTGCCCATCTCTGGGCTT 182
 QY 67 ThrLeuIleTrrPyrTrpThrArgGlnAspArgAspLeuGluProIleAsnPheArg 86
 Db 183 ACCCTATCTGTAAGTGAAGCAGGACAGGAGAGCCGAGCCCATTAATCTTCGCG 242
 QY 87 LeuProGluAsnArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeu 106
 Db 243 CTCACAGAGATGCAATGAG 302
 QY 107 AsnAspThrGlyAsnTyrTrpCysMetLeuArgAsnThrTyrCysSerLysValAla 126
 Db 303 AATGACACGGGCAATTAACCTGATCTTGAAGAACCACTTAATGACACAGATTGCA 362
 QY 127 PheProLeuGluValValGlnLysAspSerCysPheAsnSerProMetLysLeuProVal 146
 Db 363 TTTCCCTCGAAGTGTTCAG 422
 QY 147 HisLeuLeuTrrIleGlyTrrGlyIleGlnArgIleThrCysProAsnValAspGlyTrr 166
 Db 423 CACAGAGATGATATGAAACATGATTCATGATGATGATGATGATGATGATGATGATGAT 482
 QY 167 PheProSerSerValLysProThrIleThrTrrPyrMetGlyCysTrrLysIleGlnAsn 186
 Db 483 TTTCTCTTCAGTGTGACATGACATGACATGACATGACATGACATGACATGACATGACAT 542
 QY 187 PheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsn 206
 Db 543 TTTTCATATCTACTACACAGGAGCATGATGATGATGATGATGATGATGATGATGATGAT 602
 QY 207 AsnGlyAsnTrrThrCysValValAlaThrTrrProGluAsnGlyArgThrPheHisLeuTrr 226
 Db 603 TACGGCATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662
 QY 227 ArgThrLeuThrValLysValValGlySerProLysAsnAlaValProPro-----Val 244
 Db 663 ANACATGTGATCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721
 QY 245 IleHisSerProAsnAspHisValValTrrGlyLysGluPro 258
 Db 722 CTC-----AATGACCGTGTGTATAGAA---GAACCA 751
 RESULT 8
 LOCUS B1331848 888 bp mRNA linear EST 30-JUL-2001
 DEFINITION 602882528F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5135287 5',
 mRNA sequence.
 ACCESSION B1331848
 VERSION B1331848.1 GI:15016505
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 1 (bases 1 to 888)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LLM11332 row: h column: 08
 High quality sequence stop: 802.

FEATURES

source
 1..888
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5135287"
 /clone_lib="NCI CGAP_L19"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: liver; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP library."
 BASE COUNT 217 a 227 c 219 g 225 t
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Alignment Scores:

Pred. No.: 1.55e-94 Length: 888
 Score: 989.00 Matches: 195
 Percent Similarity: 88.57% Conservative: 22
 Best Local Similarity: 79.59% Mismatches: 25
 Query Match: 26.96% Indels: 6
 DB: 13 Gaps: 2

US-10-061-727-2 (1-687) x B1331848 (1-888)

QY 1 MetThrLeuLeuTrrCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
 Db 120 ATGGGAGCTTCTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 179
 QY 21 SerGluArgCysAspAspTrrGlyLeuAspThrMetCArgGlnIleGlnValPheGluAsp 40
 Db 180 TCGGAGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 239
 QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
 Db 240 GAGCCGCGCTGAGATCAAGGCCCTCTTGAACCTTCTGAGATGATGATGATGATGATGATGAT 299
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrrPyrTrpThrArgGlnAspArgAspLeuGlu 80
 Db 300 GCCCATTCCTCGGCTTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrr 100
 Db 360 GAGCCATTAACTTCGCTCCAGAGATGCAATGATGATGATGATGATGATGATGATGATGAT 419
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrrCysMetLeuArgAsnThr 120
 Db 420 TTCGGGCCACCTCTCATATGACAGGCAATTAACCTGATGATGATGATGATGATGATGATGAT 479
 QY 121 TrrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
 Db 480 TACTGAGCAAGTTCGATTTCCCTGGAAGTGTTCAGAGAGACAGCGTTTCAATCT 539
 QY 141 ProMetLysLeuProValHisLysLeuTrrIleGlyTrrGlyIleGlnArgIleThrCys 160
 Db 540 GCCATGAGATTCACAGTGCACAAAGATGATTAATGAAATGATGATGATGATGATGATGATGAT 599

QY 161 Pro-AsnValAspGlyTyrPheProSerServalysProThrIleThrTrpIleMetG1 180
|||
Db 600 CCAAAATGTAAGCGAATCTTCTTCCAGTCAACCACTGGCTCCTGGTAAGG 639
|||
QY 180 YQsTYrLYsIleGlnAsnDheAsnValIleProGluGlyMetAsnLeuSerPhele 200
|||
Db 660 TTGTACTGAATAGTACTTTCAT-AATGTACTACCGAGGCGATGAACTTGAGCTTTC 718
|||
QY 200 uIleAlaLeuIleSerAsnValIleProGluGlyMetAsnLeuSerPhele 219
|||
Db 719 -ATCCCTTGTTCAATACAGG-AATACACATGTTGTTACCAATATCTTGAAA 776
|||
QY 219 nGlyArgThrPheHisLeuThrArgThrLeuThrValValGlySerProLysAs 239
|||
Db 777 CCGGACCGTCTTTCACCTCAGATGATGACTGTAGG---TTGTGTATCCAAAGCA 833
|||
QY 239 nAlaValProPro 243
|||
Db 834 ATGCTGCCCCCA 846
|||
RESULT 9
992231 BE892231 910 bp mRNA linear EST 20-OCT-2000
US 601435065F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920152 5',
--FINITION mRNA sequence.
ACCESSION BE892231
KEYWORDS BE892231.1 GI:10352355
SOURCE EST.
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 910)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DMP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9751 row: a column: 17
High quality sequence stop: 710.
Location/Qualifiers
1..910
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3920152"
/clone_id="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT; Site_1: NCI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 236 a 241 c 210 g 223 t
ORIGIN
Alignment Scores:
Pred. No.: 6,84e-88 Length: 910
Score: 927.00 Matches: 190
Percent Similarity: 78.31% Conservative: 5
Best Local Similarity: 76.31% Mismatches: 25
Query Match: 25.27% Indels: 31
DB: 12 Gaps: 1
US-10-061-727-2 (1-687) x BE892231 (1-910)
QY 1 MetThreuleuTrpCyValValSerLeuTyPheTyGlyIleLeuGlnSerAspAla 20
|||
Db 183 ATGACACTTCTGTGTGTACTAGTCTCTACTTTATGATCCTGAAATGATATGCC 242
|||
QY 21 SerGluArgCyAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
|||
Db 243 TGAAGACGTCGATGATACGCGAGCATAGACACATGAGGCAATCCAAATGTTTGAAGAT 302
|||
QY 41 GluProAlaArgIleIleGlySerProLeuPheGluHisPheLeuIlePheSerThr 60
|||
Db 303 GAGCAGCGTCGATGATGAGCCACTCTTGAACCTTTGAATTCATCTACAGCACA 362
|||
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpIleTrpThrArgGlnAspArgAspLeuGlu 80
|||
Db 363 GCCCATTAAGCTGGCTTACTCTGATCTGTATGAGACTAGGACAGACCGGACCTTGAG 422
|||
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerGlyLeuLysAspValLeuTrp 100
|||
Db 423 GAGCCAAATTAATCTTCGCTCCCGAGAACCCGATTAAGAGAGAAATGCTGTGG 482
|||
QY 101 PheArgProThrIleLeuLeuAsnAspThrGlyAsnTrpThrCysMetLeuArgAsnThr 120
|||
Db 483 TTCCGCGCCACTCTCTCAATGACACTGGCACTATACCTGATGTTAAGAACACTACA 542
|||
QY 121 TyrcysSerIleValAlaPheProLeuGluValValGlnLysAspSerCysPhe-AsnSe 140
|||
Db 543 TATTCAGCAAGTT-GCAATTCCTTGAGAGTTGTTCAAAAGACAGCTGTTCAAAATTC 601
|||
QY 140 rPrometLysLeuProValHisIleLys-LeuTyrlleGluTyrlleGlyIleGlnArgIleThr 159
|||
Db 602 CCCCATGAAGACTCCAGTCATTAACCTGTATATGAATATGGCATTCAGAGATCACT 661
|||
QY 160 CyPProAsnValAspGlyTyrPheProSerServalysProThrIleThrTrpIleMet 179
|||
Db 662 TGTTCATGATGTGATGATATTTCTTCCAGTGT-AAACCACTATATCACTTGATTAAG 720
|||
QY 180 GlycysTYrLYsIleGlnAsnDheAsnValIleProGluGlyMetAsnLeuSerPhe 199
|||
Db 721 GCCTGTATTAATAATACGACATTTTC----- 744
|||
QY 200 LeuIleAlaLeuIleSerAsnValIleProGluGlyMetAsnLeuSerPhe 219
|||
Db 745 -----ATATGTATACCGAAGTT 762
|||
QY 220 GlyArgThrPheHisLeuThrArgThrLeuThrValLysValGlySerProLysAsn 239
|||
Db 763 GACCTGAGTCCCATGCTTAATGACATTATGATGATGATGATGATGATGATGATG 822
|||
QY 240 AlaValProProValIleHis 246
|||
Db 823 GACATTTCTTCCAGACCGCAT 843
|||
RESULT 10
B1346913 580 bp mRNA linear EST 30-JUL-2001
LOCUS B1346913
DEFINITION 376288 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION B1346913
VERSION B1346913.1 GI:15040211
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 580)
AUTHORS Fahnenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,B.,
Stone,R.T., Heaton,M.P., Grose,W.M., Bennett,G.A., Laegreid,W.W.,
and Keeler,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366

Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.

PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCACGACGACG
 Plate: 130 row: L column: 3
 Seq primer: ATTGAGTGCACCTATG.

FEATURES
 Location/Qualifiers
 1..580

/organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC 2Pig"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
 library made from pooled tissue from testis, ovary,
 endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 159 a 110 c 158 g 153 t
 ORIGIN

Alignment Scores:

Pred. No.: 5.67e-87 Length: 580
 Score: 915.00 Matches: 185
 Percent Similarity: 97.44% Conservative: 5
 Best Local Similarity: 94.87% Mismatches: 3
 Query Match: 24.94% Indels: 3
 DB: 13 Gaps: 1

US-10-061-727-2 (1-687) x B1346913 (1-580)

QY 309 AepglutThrArgThrGlnIleuSerIleuValThSerGlnuSpleuLysArg 328
 Db 3 GATGAGACAGACCTCAGCTTTGACATCAAGAGACTA-CTGCTGAGATCTCAAGCCG 61
 QY 329 SerTyrValCysHisAlaArgSerIleuValGlnValAlaLysAlaLysVal 348
 Db 62 AACTATGCTGTCATGCCAGAAATGCCAAGGAGGAGTTGACACCGCCGCAAGGAGAA 121
 QY 349 GlnLysValProAlaProArgTyrThrValGlnLeuAlaCysGlyPheGlnAlaThrVal 368
 Db 122 CAGAAA-----GCTCCGAGATACACAGTGAAGTGGCATGTGGTTTGGAGCACAAGTC 175
 QY 369 LeuLeuValValIleuLeuValValIleuValIleuValIleuValIleuValIleuVal 388
 Db 176 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 235
 QY 389 TyrArgAlaHisPheGlyThrAspGluThrIleuAspGlyLysGluTyrAspIleuTyr 408
 Db 236 TATCGGCTCATTTTGGAAACAGATGAACCATTTTGAATGGAGAAATATGATTTAT 295
 QY 409 ValSerTyrAlaArgAsnAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 428
 Db 296 GATATCTATGACAGAGATCTGAGAGAGAGATTTGATTTATCTACCTCCGTGAGATC 355
 QY 429 LeuGlnAsnGlnPheGlyTyrIleuValCysIleuPheAspArgAspSerLeuProGlyGly 448
 Db 356 TTGGAGATGAATTCGAGATCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
 QY 449 AenThrValGlnAlaValPheAspPheIleGlnArgSerArgArgMetIleValIleuVal 468
 Db 416 AATACGGTGAAGAGAGTTTGAATCTTCAATCAAGAGAGCGGAGAGAGATGTGCTG 475
 QY 469 SerProAspTyrValThrGlnLysSerIleSerMetLeuGlnPheLysLeuGlyValMet 488
 Db 476 AGCCAGAGCTATGATGACAG 535
 QY 488 CysGlnAsnSerIleAlaThrLysLeuIleValGlnTyrArg 503
 Db 536 TGCCAAATCCATTCGACCAAGAGCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 580

RESULT 11
 AV656295 596 bp mRNA linear EST 16-JAN-2002
 LOCUS AV656295 GLC Homo sapiens cDNA clone GLCERH02 3', mRNA sequence.
 DEFINITION AV656295
 ACCESSION AV656295
 VERSION AV656295.1 GI:9877309
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 596)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z., and Han, Z.

TITLE
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106

JOURNAL MEDLINE

COMMENT
 Contact: Zenguan Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@hgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers
 1..596

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 /lab_host="SOLR"
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 XhoI"

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 ORIGIN

Alignment Scores:

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 Query Match: 24.53% Indels: 0
 DB: 10 Gaps: 0

US-10-061-727-2 (1-687) x AV656295 (1-596)

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 Db 10 GCGCTTTAAATAATACAGAAATTTAATATATATATATATATATATATATATATATAT 69
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 Db 130 GAGCTATGCTTCACTACACAGACTCTGACTTAAGAGTGAAGGCTCTCCCAAAAAT 189
 QY 240 AlaValProProValIleHisSerProAsnAspHisValValTyrGlnLysGlnProGly 259
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QY 280 ValTrrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsn 299
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 QY 300 GluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 319
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 JN BM760155.1 GI:19089770
 WORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.krdb.re.kr
 Plate: 14 row: A column: 03
 High quality sequence stop: 489.

FEATURES
 Source
 Location/Qualifiers
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 /cell_line="SNU-668"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was decapped with tobacco
 acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
 including EcoRI site by treatment of T4 RNA ligase. The
 first strand cDNA was synthesized from oligo dT-selected
 mRNA by priming with dT-tailed vector. The dT-tailed
 vector was adjusted to have about 60nt. The cDNA vector
 was circularized with E. coli DNA ligase after digestion
 of EcoRI which site is also included in vector. An RNA
 strand converted to a DNA strand by Okayama-Berg method.
 The obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 After analyzing and sequencing about 2,000 ~ 3,000
 colonies in original cDNA library, the abundant cDNAs were
 selected and amplified by PCR reaction using vector region
 primer including T7 promoter as 5' primer and N(dT)14 as
 3' primer. The PCR products were used as template for
 synthesis of biotinylated single stranded RNA by in vitro
 transcription reaction. The synthesized RNA probes were

hybridized with antisense single stranded cDNAs prepared
 from original library and incubated with avidin-gel.
 After removing DNA-RNA hybrids by centrifuge, the
 subtracted cDNA libraries were constructed by
 transformation of the remaining DNA into competent cells E.
 coli Top10F with electroporation method."

BASE COUNT 158 a 90 c 97 g 144 t
 ORIGIN
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 Pred. No.: 6.07e-83 Length: 489
 Score: 876.00 Matches: 162
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 23.88% Indels: 0
 DB: 14 Gaps: 0
 US-10-061-727-2 (1-687) x BM760155 (1-489)
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 DB 3 AGATCACTTGCCAAAGATGATGATATTTCCCTCCAGTCCAAACCACTATCACT 62
 QY 177 TrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsn 196
 DB 63 TGGTATATGGCTGTATTAATAATACAGAAATTTATATATGTAATACCCGAAAGTATGAC 122
 QY 197 LeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyr 216
 DB 123 TTGAGTTTCCCATTCAGCTTATATCAATATATGAAATTCACATGTTGTTACATAT 182
 QY 217 ProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySer 236
 DB 183 CCAGAAATGACAGTACGTTTCATCTCCACGACTCGACTGTAAAGTATGAGGCTCT 242
 QY 237 ProLysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGluLys 256
 DB 243 CCNAAATATGAGATCCCTCGTATATCATTCACCTATATGATCATGTGCTTATAGAAA 302
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 QY 277 ArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspVal 296
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 QY 297 ThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeu 316
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 QY 317 SerIle 318
 DB 483 AGCATC 488
 RESULT 13
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 DEFINITION mw96b02.t1 Soares mouse MML Mus musculus cDNA clone IMAGE:678507 5'
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 accessory (MUSE);, mRNA sequence.
 ACCESSION AA237107
 VERSION AA237107.1 GI:1861163
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 598)
 AUTHORS Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B.,
 Meising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

[illegible]

computer-based methods for the mouse full-length cDNA encyclopedic: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001).

Yamada, I., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arkawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct. Func. Genomics* 2 pre, 172-186 (2001).

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

mouse tissues.

FEATURES							
Location/VNAligner							
SOURCE							
<pre>1 . 652 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="933013B06" /clone_1lb="RIKEN full-length enriched, adult male diencephalon" /sex="male" /tissue_type="diencephalon" /dev_stage="adult" /lab_host="DH10B" /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'] GAGAGAGAAGATCCACGAAGCTTTTATTTCCTTTTAA 3'}. cDNA was transcribedase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGAATTCGTCAAGTAATAAATTAATCCCCCCC 3'}. cDNA was cloned into the XbaI(+) after blunt excision Vector: a modified pBluescript KS(+)</pre>							
<p>BASE COUNT 153 a 171 C 168 g 159 t 1 others ORIGIN BamHI"</p>							
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<p>US-10-061-727-2 (1-687) x BB625831 (1-652)</p>							
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Db	133	ATGGAGACTTGCGTGATTTGGATGAGCTGCTCATATGGANCTCGAGAGTCAGTCT	192				
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OY	61	AlahiseraiaagyleuthrileultetryrtThraRarginaspaRGAspleuglu	80				
Db	313	GCCCATTCCTCTGGCTTACCCTGATCTGGATCGAGCACGGCAAGACCGGAGCTGGAG	372				
OY	81	GluProIleasnPheArgleuprogluasnaraglisertrysgulyasppalleutr	100				
Db	373	GAGCCACTTAATCTCCGCTCCAGAGAAATCGATCACTAAGAGAAAATGTGCTCTGG	432				

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Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
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Qy 121 TyrCysSerIysValAlaPheProLeuGluValValGlnIysAspSerCysPheAsnSer 140
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Qy 141 ProMetIysLeuProValHisIysLeuTyrIleGluTyrGlyIleGlnArgIlePheCys 160
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Db 553 GCCATGAGATTCCCAAGTGCACAGATGTAATGTAACATGGCATTCATTAAGATCAGATGT 612
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Qy 161 ProAsnValAspGlyTyrPheProSerSerValIysPro 173
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Db 613 TCAATGTAGAGGATCTTCTTTCAGTGTCAACCA 651
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 job time : 1684 secs

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 06:44:49 ; Search time 3717 Seconds

(without alignments)
16160.396 Million cell updates/sec

Title: US-10-061-727-1

Perfect score: 2064

Sequence: 1 atgacactctctgctgctgtc.....acgactttatccatataa 2064

Scoring table: IDENTITY NUC
Gap 10.0 , Gape 1.0
2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seg length: 0
Maximum DB seg length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pt:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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19: em_mu:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
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34: em_htg_pln:*
35: em_htg_rod:*
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38: em_sy:*
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40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1388.4	67.3	1740	6	ARI66115 Sequence
2	1388.4	67.3	1740	9	AF029213 Homo sapi
3	1388.4	67.3	1740	9	AB006537 Homo sapi
4	1067.4	51.7	3355	6	ARI66116 Sequence
5	1067.4	51.7	3355	10	MM11RACP
6	1051	50.9	1857	9	AF167343 Homo sapi
7	1049.8	50.9	1857	10	RNT48592
8	793.4	38.4	1916	10	BC021159 Mus muscu
9	776.4	37.6	2226	9	AK095107 Homo sapi
10	718.4	34.8	46509	9	AC108747 Homo sapi
11	515	25.0	58987	2	AC119283 Mus muscu
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13	292.8	14.2	184203	9	AC008249 Homo sapi
14	248.2	12.0	87015	2	AC098400 Rattus no
15	199	9.6	548	9	AF016261 Homo sapi
16	199	9.6	594	9	AF167335S05
17	168	8.1	311	9	AF167335S06
18	153.8	7.5	2102	9	AF167335S09
19	151	7.3	2061	6	ARI79668 Sequence
20	151	7.3	2061	9	AF212016 Homo sapi
21	151	7.3	3080	9	AF167335S08
22	149.4	7.2	2080	9	HS290436 Homo sapi
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24	147.8	7.2	2212	9	AF284436 Homo sapi
25	146.8	7.1	2722	9	AF181284 Homo sapi
26	146	7.1	1979	9	AF181285 Homo sapi
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28	145.2	7.0	3504	9	HS243874 Homo sapi
29	144.4	6.8	1737	6	ARI79667 Sequence
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31	136.6	6.6	2518	10	AF284437 Mus muscu
32	115.2	5.6	87015	2	AC098400 Rattus no
33	113.6	5.5	443	6	AX410972 Sequence
34	112.6	5.5	58987	2	AC119283 Mus muscu
35	93.2	4.5	2028	10	MM0277831
36	89.6	4.3	1626	6	AR016447 Sequence
37	88.6	4.3	1991	6	ARI79676 Sequence
38	88	4.3	3522	9	HS043672 Human putat
39	75.2	3.6	1563	6	ARI02820 Sequence
40	75.2	3.6	1563	6	E26332 Polypeptide
41	75.2	3.6	1620	6	ARI02826 Sequence
42	75.2	3.6	1620	6	E26338 Polypeptide
43	75	3.6	343	9	AF167335S07 Homo sapi
44	73	3.5	1557	6	ARI02821 Sequence
45	73	3.5	1557	6	E26333 Polypeptide

ALIGNMENTS

RESULT 1
LOCUS ARI66115 1740 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6280955.
ACCESSION ARI66115
VERSION ARI66115.1 GI:16241289
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1740)
TITLE Cao, Z.
JOURNAL Interleukin-1 receptor accessory proteins, nucleic acids and
methods
Patent: US 6280955-A 1 28-AUG-2001;

Db 1527 GACCGAGACGCTGCTGGGGAAATTTCAAGATGAGACTTGAAGCTTCAATTCAGAA 1586
Qy 1381 AGCAAGAGATGATGTTGTTCTGAGCCCTGACATGATGACGAAAGAGCATCAGATG 1440
Db 1587 AGCAGACCCCTCTGCTGTTGTTCTAGCCCTCACTAGCTCAGAGGAAACCAAGCTTC 1646
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Qy 1498 GTTAGATCCCTCCCTTGAGACCCGACCCAGGCAATTTCTAGCTCAAAAGATCTGTG 1557
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1767 CTCACGGCTAATTAATGAAAGGAGGAAATCAAGTATCCACAGGGGAGGTTCTGAGAG 1826
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RESULT 4
AR166116 3355 bp DNA linear PAT 17-OCT-2001
LOCUS AR166116
DEFINITION Sequence 3 from patent US 6280955.
ACCESSION AR166116
VERSION AR166116.1 GI:16241290
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3355)
AUTHORS Cao, Z.
TITLE Interleukin-1 receptor accessory proteins, nucleic acids and methods

JOURNAL Patent: US 6280955-A 3 28-AUG-2001;
FEATURES Location/Qualifiers

source 1..3355
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ORIGIN /organism="unknown"

Query Match 51.7%; Score 1067.4; DB 6; Length 3355;
Best Local Similarity 78.9%; Pred. No. 2.3e-286;
Matches 1298; Conservative 0; Mismatches 341; Indels 6; Gaps 2;

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Db 195 TCGAAGGCTGTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 254
Qy 121 GAGCAGCTGATCAAGTGTGCACTCTTTGAACATTTCTGAAATTCATCAAGACACA 180
Db 255 GAGCGGCTGATCAAGTGTGCACTCTTTGAACATTTCTGAAATTCATCAAGACACA 314
Qy 181 GCCCATTCAGCTGCTTACTCTGATCTGTATGTGAGTGTGAGTGTGAGTGTGAGT 240
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Db 675 TGTATTAATATACGAATTTTATATATATATATATATATATATATATATATATAT 734
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Qy 901 AGTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
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Db 1335 GATGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1394
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Qy 1321 GAGCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1455 GAGCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1514
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FEATURES	source
gene	1.1862
CDS	1.1862
REFERENCE	Submitted (06-FEB-1996) Changlu Liu, Molecular Biology, Neurocrine Biosciences, Inc., 3050 Science Park RD, San Diego, CA 92121, USA
JOURNAL	Location/Qualifiers
FEATURES	1.1862
source	/organism="Rattus norvegicus"
gene	/db_xref="taxon:10116"
CDS	1.1862
REFERENCE	/gene="IL-1"
JOURNAL	103.1815
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gene	/product="interleukin-1 receptor accessory protein"
CDS	/protein_id="AA03502.1"
REFERENCE	/translation="MGLPWCMLSLFFCGILSHSERCDDWGLDTMROIQVEFEDPAP
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FEATURES	PVLADGIVNTYCMLENTYTKSVAPLEVQKDSFGNSPMRLPYRLYIEGIIHITCT
source	PLVDGVPSSVKSVDYWKYKGTCEIVNFHNVODKGNLSFPIPLVNNNGNVCVATYLE
gene	NRLHLRTMTVTKVGVGSKDVAVPHVYSIPNDRYVYKEDEBELYIPKYYPSFIMDS
CDS	HNELMTIDGKRPDVPDITITYESVYSISDETRTILSLIKTVPDLKRVYCH
REFERENCE	NRABGEABDAVKVKKVLPRTIVELACGSGATVPLVVALLIVYHVMLEVLFRAL

[illegible]

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Db 1003 AGCGTAAGTATTTCTTCAACGAGAGATGAGACAAAGACTCAGATTTTGGACATCAAGAAA 1062
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Db 1723 CAGCTGAGGTGCGCATGCGCAGTGA 1747

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RESULT 8
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LOCUS Mus musculus, similar to interleukin 1 receptor accessory protein,
DEFINITION clone MGC:14036 IMAGE:4161899, mRNA, complete cds.
ACCESSION BC021159 GI:18088147
VERSION BC021159.1
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.

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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL Submitted (07-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA

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```

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov

```

Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahy, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAX Plate: 18 Row: 1 Column: 21
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6680420.

FEATURES

source

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CDS

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BASE COUNT 594 a 399 c 420 g 503 t
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Best Local Similarity 84.7%; Pred. No. 2.5e-217;
Matches 890; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

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Db 193 TCGAGAGCTGTGATGATGACTGGGAGCTAGACACCATGAGGCAAAATCCAAAGTGTGAAGAT 252
Qy 121 GAGCAGCTGCGATGAAAGTCCCACTCTTTGAAACCTCTTGAATTCACATACAGACGA 180
Db 253 GAGCGGCTGGAATCAAGTCCCTCTTTGAAACCTCTTGAATTCACATACAGACGA 312
Qy 181 GCCATTCAGTGGCTTACTCTGATCTGTATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 313 GCCATTCAGTGGCTTACTCTGATCTGTATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
Qy 241 GAGCATAATTAATCTCGCTCCCGAGAGACCGCATTAAGTAAAGAGAGAGAGAGAGAGAGAGAG 300
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Qy 361 TATTCGAGCAAGTGTGATTTCCCTTGAAGTGTTCAAAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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 Db 853 TTGCCCCCTGAT 912
 Oy 781 GAGTATGAT 840
 Db 913 GAGTATGAT 972
 Oy 841 TGTGATGAT 900
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 Oy 901 AGTATATGAT 960
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 Db 1093 GTTATCTGAT 1152
 Oy 1021 GTTATCTGAT 1051
 Db 1153 GTTATCTGAT 1183

RESULT 9
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 LOCUS Homo sapiens cDNA FLJ37788 f1s, clone BRHIP2028593, weakly similar
 DEFINITION to Homo sapiens IL-1 receptor accessory protein mRNA.
 ACCESSION AK095107
 VERSION AK095107.1 GI:21754300
 SOURCE Homo sapiens; tissue: testis (full insert sequence).
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1
 Nomenclature: Magatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
 Kodaira, H., Katsuya, T., Takahashi, M., Kikkawa, B., Omura, Y., Abe, K.,
 Kamihara, K., Katsuya, T., Sato, K., Tanikawa, M., Yamazaki, M.,
 Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
 Yamamoto, J., Isono, Y., Kawai, H., Kawai, H., Saito, K., Nishikawa, T.,
 Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
 Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi, F., Fujii, A.,
 Ohnaka, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
 Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
 NEDO human cDNA sequencing project
 TITLE Unpublished
 REFERENCE 2 (bases 1 to 2226)
 AUTHORS Isogai, T. and Yamamoto, J.
 JOURNAL Direct Submission
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

COMMENT
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.
 Location/Qualifiers
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 BASE COUNT 629 a 480 c 509 g 608 t
 ORIGIN
 Query Match 37.6%; Score 776.4; DB 9; Length 2226;
 Best Local Similarity 99.7%; Pred. No. 2, 1e-212;
 Matches 777; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Oy 1346 ATACATGATGATGATATGATATGATATGATATGATATGATATGATATGATATGATAT 1405
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 Oy 1406 GCCCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1465
 Db 121 GCCCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Oy 1466 GCCAGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1525
 Db 181 GCCAGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Oy 1526 ACCAGGATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1585
 Db 241 ACCAGGATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 Oy 1586 CCAAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1645
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 Oy 1646 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1705
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 Oy 1706 ACGTTCAAG 1765
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[illegible]

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TITLE      Direct Submission
JOURNAL    Submitted (31-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA

REFERENCE   3 (bases 1 to 46509)
AUTHORS    Morley,K.C.
TITLE      Direct Submission
JOURNAL    Submitted (03-JUN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            4 (bases 1 to 46509)
            Morley,K.C.

REFERENCE   4 (bases 1 to 46509)
AUTHORS    Morley,K.C.
TITLE      Direct Submission
JOURNAL    Submitted (21-JUN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On Jun 21, 2002 this sequence version replaced gi:21306532.
COMMENT     INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402), similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot
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Best Local Similarity 99.7%; Pred. No. 1.7e-195;
Matches 719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| | | | |
QY 1404 GAGCCCTGATATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463
| | | | |
DB 22900 GAGCCCTGATATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 22959
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QY 1464 GTCAG 1523
| | | | |
DB 22960 GTCAG 23019
| | | | |
QY 1524 GCACCCAG 1583
| | | | |
DB 23020 GCACCCAG 23079
| | | | |
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DB 23200 TCACGTTCAAG 23259
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DB 23260 GGTTCAG 23319
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QY 1824 CACCTGCGAG 1883
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QY 1884 GGCAG 1943
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DB 23380 GGCAG 23439
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QY 1944 GTGAG 2003
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DB 23440 GTGAG 23499
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DB 23500 AGCCCTGCTCTTCAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 23559
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QY 2064 A 2064
DB 23560 A 23560

RESULT 11
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LOCUS AC119283
DEFINITION Mus musculus clone RP24-345H5, LOW-PASS SEQUENCE SAMPLING.
AC119283
ACCESSION AC119283
VERSION AC119283.1 GI:20304009
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 58987)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP24-345H5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 58987)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

TITLE
JOURNAL
COMMENT

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhvalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Farro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
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McClerny, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,
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Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunthang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Salt, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L25964

Center clone name: 345_H_5

* NOTE: This record contains 72 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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* 1552 1651: gap of 100 bp
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Version: 1.01 gxfco.

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 Best Local Similarity 97.7%; Pred. No. 1.4e-72;
 Matches 297; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 Db 153275 CAGAACGCTGCATGACTGGGAGCTAGACACCATGAGGCAATTCAGTCTTGAAGATG 153334
 Qy 122 AGCCAGCTGCATGACTGAGTCCCATCTTTGACACTTTTGAATTAATCAACGACAG 181
 Db 153335 AGCCAGCTGCATGACTGAGTCCCATCTTTGACACTTTTGAATTAATCAACGACAG 153394
 Qy 182 CCATTCAGTGCCTTACTCTGATCTGATCTGATTTGAGACTAGGACCGGACCTTGAGG 241
 Db 153395 CCATTCAGTGCCTTACTCTGATCTGATCTGATTTGAGACTAGGACCGGACCTTGAGG 153454
 Qy 242 AGCCATTAACCTTCCGCTCCCGAGAACCGCATTTAGTAGAGAAAGATGCTGTGTG 301
 Db 153455 AGCCATTAACCTTCCGCTCCCGAGAACCGCATTTAGTAGAGAAAGATGCTGTGTG 153514
 Qy 302 TCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGACATTTAAGGACACTACAT 361
 Db 153515 TCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGACATTTAAGGACCTGAT 153574
 Qy 362 ATTG 365
 Db 153575 CTTG 153578

RESULT 14
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 49 unordered pieces.
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 VERSION
 HTG: HTGS_PHASE1.
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 1 (bases 1 to 87015)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaraltinge,H.C., Are,J.R., Ayele,M., Banks,T.,
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 Cleveland,C.D., Cox,C., Coyte,M.D., Dathorne,S.R., David,R.,
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 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
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 Rivers,M., Rojas,A., RojudoKan,I., Rolfe,M., Ruiz,S., Savary,G.,
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLES
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AUTHORS
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JOURNALS
COMMENT

Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
Unpublished
2 (bases 1 to 87015)
Morley, K. C.
Direct Submission
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 87015)
Morley, K. C.
Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 24, 2002 this sequence version replaced gi:16328167.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: TUPS
Center clone name: CH230-2B16
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Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 1000 of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 45081 bases at least Q40
Consensus quality: 48248 bases at least Q30
Consensus quality: 50450 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 49 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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FEATURES
source

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Matches 280; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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VERSION AF016261.1 GI:2911297
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 548)
AUTHORS Dale, M., Hammond, D. W., Cox, A. and Nicklin, M. J.
TITLE The human gene encoding the interleukin-1 receptor accessory protein (IL1RAP) maps to chromosome 3q28 by fluorescence in situ hybridization and radiation hybrid mapping
JOURNAL Genomics 47 (2), 325-326 (1998)
MEDLINE 98140136
PUBMED 9479509
REFERENCE 2 (bases 1 to 548)
AUTHORS Dale, M., Cox, A. and Nicklin, M. J. H.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1997) Department of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield S10 2UF, United Kingdom
COMMENT On Feb 26, 1998 this sequence version replaced gi:2909774.
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OY 514 AAACCGACTATCACTGGTATATGAGCTGTATATTAATAATACGAATTTTAAAT 564
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Search completed: April 30, 2003, 09:15:23
Job time : 4260 secs


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Db 1021 GCTAGAGAGCTGCGCAAGTGAACAGAAAGTCAATACCAAGATGACAGTGAATC 1080
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Db 1081 GCGGTGTGTTTGGAGCCAGCTCTTCTGTGTGTGTTCTGATTTGTATTCATGTT 1140
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Qy 1321 GACCGAGACAGTCTGCTGCGGGAATACAGTGAAGCAGTTTGTATTTCAATTCAGAGA 1380
Db 1321 GACCGAGACAGCTGCTGCGGGAATATGTACAGATGACACCTGAGCTTCATTCAGAAA 1380
Qy 1381 AGCAGAGAGATGATGATTTGTTCTGAGCCCTGACTGATGACAGAAAGAGATCAGATG 1440
Db 1381 AGCAGAGAGATCTCTGTTGTTCTTAAGTCCCACTAGCTGCTCCAGGAGACAGACCTTC 1440
Qy 1441 CTGAGATTTAACTGAGTGTATGTCAGAACTCCATTTG---CCACCAAGCTCATTTGT 1497
Db 1441 CTGAGATCTCAAGCTGAGCTCAGAAATATGAGCTCCCGGAGCAATCAAGCTCATTTTA 1500
Qy 1498 GTTGAAGTACCGTCCCTTGAAGCACCAGCCAGCAAGCTTCTTCACTCAAGAGTCTGTG 1557
Db 1501 GTGCAAGTACCAAGCTGGAAGCATGAGTGAAGAGCTGAAGCGGCTGAAGACGCTG 1560
Qy 1558 ---TCTTTGTGAGCTGGAAGGAGAAAGTCCAAACATTTGCTTAATTTCTGAAA 1614
Db 1561 CTCACGCTCAATTAATGAAAGAGAGAAATCCAAATGATCTCTCAGGCGAGGTTCTGAG 1620
Qy 1615 GCTTTCGCTTGGCTCTTCCCTCTGA 1639
Db 1621 CAGTTGACGTTGGCAGTCCAGTGA 1645

kBSULT 6
ID AAS15609 standard; cDNA; 3355 BP.
XX AAS15609;
AC AAS15609;
XX
DT 21-MAY-2002 (first entry)
XX
DE Mouse interleukin-1 Receptor accessory protein (IL-1R ACP) cDNA.
XX
KW IL-1R ACP; mouse; interleukin-1 receptor accessory protein; NF-kappaB;
XX IL-1; IL-1R; ss; inflammatory response.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 135..1847
FT /tag= a
FT /product= "interleukin-1 receptor accessory protein"
XX
PN US6280955-B1.
XX
PD 28-AUG-2001.
XX
PF 16-DEC-1997; 97US-0991944.
XX

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PR 16-DEC-1997; 97US-0991944.
XX
PA (TUL-1) TULARIK INC.
XX
PI Cao Z;
XX
DR WPI; 2001-595441/67.
DR P-PSDB; AAU09967.
XX
PT Isolated polypeptide designated interleukin receptor accessory
PT polypeptide is useful for regulating cell function
XX
PS Example; Fig 2; 21p; English.
XX
CC This sequence represents the mouse interleukin-1 receptor accessory
CC protein (IL-1R ACP) cDNA that was used to generate a cDNA fragment
CC used as a hybridization probe to isolate, from a cDNA library,
CC the human IL-1R ACP cDNA of the invention. The interleukin receptor
CC accessory protein (IL-1R ACP) and its modulators (agonists/antagonists)
CC are useful for regulating cell function. Transient expression of either
CC IL-1R or IL-1RACP alone does not result in ligand-independent induction
CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
CC coexpression of both proteins resulted in a 20-fold increase in
CC activation of NF-kappaB activity to a level comparable to that induced
CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1R ACP as
CC a result of protein overexpression can elicit a signaling pathway
CC leading to NF-kappaB activation. Modulating signal transduction
CC involving NF-kappaB in a cell may be achieved by modulating the activity
CC of IL-1RACP using binding agents such as agonists and antagonists.
CC Hybridization probes to the cDNA sequence can be used to identify wild-
CC type and mutant IL-1R ACP alleles in clinical and laboratory
CC samples. Mutant alleles are used to generate allele-specific
CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
CC of diseases or disorders with an inflammatory response. In
CC therapy, therapeutic IL-1RACP nucleic acids are used to modulate
CC cellular expression or intracellular concentration or availability of
CC active IL-1R ACP. This invention also comprises a method of screening for
CC an agent that modulates the interaction of an interleukin receptor
CC accessory polypeptide (IL-1R ACP) to a binding target.
XX
SQ Sequence 3355 BP; 909 A; 742 C; 753 G; 951 T; 0 other;
Query Match 51.7%; Score 1067.4; DB 23; Length 3355;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 1298; Conservative 0; Mismatches 341; Indels 6; Gaps 2;
Qy 1 ATGACACTTCTGTGATGTAGTACGTCTTAATTTATGAAATCTGCAAGATGCC 60
Db 135 ATGGAATCTCTGTGATTTGATGATGATCTGTCTTATGAGATCTGCAAGATGCT 194
Qy 61 TCAGAAAGCTGCGATGATCGGGAGCTAGACACCATAGGCAATCAAGTGTGGAAGT 120
Db 195 TCAGAGCGCTGTGATGATCGGGAGCTAGATACCATGCAATCAAGTGTGGAAGT 254
Qy 121 GAGCGAGCTGATCAAGAGCCACTCTTGAACACTTCTGTAATTAACATACAGACCA 180
Db 255 GAGCGAGCTGATCAAGAGCCACTCTTGAACACTCTGTAATTAACATACAGACCA 314
Qy 181 GCCATTAGCTGAGCTCTTACTGTATGATCTGTATGATGAGCAGGACCGGACTTTAG 240
Db 255 GAGCGAGCTGATCAAGAGCCACTCTTGAACACTCTGTAATTAACATACAGACCA 314
Qy 315 GCCATTCTCTGAGCTTACCGCTTACCGTATCTGTACAGGACCAAGCCGAGACCTG 374
Db 315 GCCATTCTCTGAGCTTACCGCTTACCGTATCTGTACAGGACCAAGCCGAGACCTG 374
Qy 241 GAGCCATTAATCTTCCGCTCTCCCGAGAACCGCATTAATGTAAGAGAAAGATGTCTG 300
Db 375 GAGCCATTAATCTTCCGCTCTCCCGAGAACCGCATTAATGTAAGAGAAAGATGTCTG 434
Qy 301 TTCCGGCCCACTCTCTCAATGACCTGCAACTTAACCTGATGTAAGAGAACTATCA 360
Db 435 TTCCGGCCCACTCTCTCAATGACCTGCAACTTAACCTGATGTAAGAGAACTATCA 494
Qy 361 TATTGAGCAAGATGATCTTCCCTTGAAGTGTTCAAAGAGACAGCTGTTCATTC 420
Db 495 TACTGAGCAAGATGATCTTCCCTTGAAGTGTTCAAAGAGACAGCTGTTCATTC 554

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QY 421 CCCATGAACTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 480
 DB 555 GCCATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 614
 QY 481 CCAATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 540
 DB 615 CCAATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 674
 QY 541 TGTATATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 600
 DB 675 TGTATATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 734
 QY 601 ATGCTATATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 660
 DB 735 ATGCTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 794
 QY 661 CCAATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 720
 DB 795 CCAATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 854
 QY 721 GTGCTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 780
 DB 855 GTGCTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 914
 QY 781 GAGTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 840
 DB 915 GAGTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 974
 QY 841 TGTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 900
 DB 975 TGTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1034
 QY 901 AGTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 960
 DB 1035 AGTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1094
 QY 961 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1020
 DB 1095 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1154
 QY 1021 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1080
 DB 1155 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1214
 QY 1081 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1140
 DB 1215 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1274
 QY 1141 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1200
 DB 1275 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1334
 QY 1201 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1260
 DB 1335 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1394
 QY 1261 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1320
 DB 1395 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1454
 QY 1321 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1380
 DB 1455 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1514
 QY 1381 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1440
 DB 1515 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1574
 QY 1441 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1497
 DB 1575 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1634

QY 1498 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1557
 DB 1635 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1694
 QY 1558 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1614
 DB 1695 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1754
 QY 1615 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1639
 DB 1755 GTTATATGAGATTCCTCCAGTGCATTAATCTGATATAGAAATGSCATTCAGAGGATCATCTGT 1779
 RESULT 7
 AA23659
 ID AA23659 standard; cDNA; 2155 BP.
 AC AAV23659;
 XX
 DT 17-AUG-1998 (first entry)
 XX
 DE Human interleukin-1 receptor accessory molecule cDNA.
 XX
 KM Interleukin-1 receptor accessory molecule; IL-1R Acm; human;
 KM signal transduction; infection; septic shock; inflammation;
 KM rheumatoid arthritis; therapy; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 303..1373
 FT /tag= a
 FT sig_peptide 303..353
 FT /tag= b
 FT mat_peptide 354..1370
 FT /tag= c
 XX
 PN M09808969-A1.
 XX
 PD 05-MAR-1998.
 XX
 PF 26-AUG-1996; 96MO-US13954.
 XX
 PR 26-AUG-1996; 96MO-US13954.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Bednarik DP, Olsen HS, Rosen CA;
 XX
 DR WPI: 1998-230267/20.
 DR P-PSDB; AAM53897.
 PT Nucleic acid encoding interleukin-1 receptor accessory protein -
 PT used for therapeutic modulation of IL-1 activity
 XX
 PS Claim 2; Fig 1; 95pp; English.
 XX
 CC This cDNA clone codes for human interleukin-1 receptor accessory
 CC molecule (IL-1R Acm) (see AAM53897), a new member of the
 CC immunoglobulin superfamily that forms a complex with type 1 IL-1R
 CC and which has higher affinity for IL-1 than the receptor itself,
 CC suggesting that the known high and low affinity forms of IL-1R are
 CC in fact the receptor with or without IL-1R Acm, respectively.
 CC The 2155 bp sequence is present in clone HMB52 (deposited as
 CC ATCC 97666) derived from microvascular epithelium (no details of
 CC isolation given). Recombinant expression in Escherichia coli,
 CC mammalian and insect cells is described. Recombinant host cells
 CC and recombinant vectors are claimed. Also claimed are isolated
 CC nucleic acid molecules encoding epitope-bearing portions (see
 CC AAM53898-915) of IL-1R Acm. Recombinant IL-1R Acm can be used to
 CC identify IL-1R agonists and antagonists useful for therapeutic
 CC modulation of IL-1 activity, and to raise specific antibodies.
 CC Nucleic acid fragments are useful as diagnostic probes and primers,


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|||||
Db 61 CAGCTGCATCAAGTCCCACTTTGAAACCTTGAATTCATCTAGACAGACGCC 120
Qy 185 ATTACGCTGGCTTACTCTGATCTGTATTGGACTAGGACCGGACCTTGAAGAGC 244
Db 121 ATTACGCTGGCTTACTCTGATCTGTATTGGACTAGGACCGGACCTTGAAGAGC 180
Qy 245 CAATTACTCTCGGCTCCCGGAGAACCGCATTAGTAGGAGAAAGATGTGCTGTTC 304
Db 181 CAATTACTCTCGGCTCCCGGAGAACCGCATTAGTAGGAGAAAGATGTGCTGTTC 240
Qy 305 GGCCCACTCTCTCAATGACACTGGCAACTATACCTGATTTAAG 351
Db 241 GGCCCACTCTCTCAATGACACTGGCAACTATACCTGATTTAAG 287

RESULT 9
AA149786
ID AA149786 standard; DNA; 287 BP.
XX
AC AA149786;
XX
Xx 17-OCT-2001 (first entry)
Dc Probe #8472 used to measure gene expression in human placenta sample.
XX
Xx Probe: microarray; human; placenta; antenatal diagnosis;
Xx genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
Xx (MOLE-) MOLECULAR DYNAMICS INC.
XX
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-48897/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 18472; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SNP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 287 BP; 76 A; 78 C; 68 G; 65 T; 0 other;
Query Match 13.9%; Score 287; DB 22; Length 287;
Best Local Similarity 100.0%; Pred. No. 7.7e-81;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 65 AACGCTGCATCAAGTCCCACTTTGAAACCTTGAATTCATCTAGACAGACGCC 124
Db 1 AACGCTGCATCAAGTCCCACTTTGAAACCTTGAATTCATCTAGACAGACGCC 60
Qy 125 CAGCTGCATCAAGTCCCACTTTGAAACCTTGAATTCATCTAGACAGACGCC 184
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|||||
Db 61 CAGCTGCATCAAGTCCCACTTTGAAACCTTGAATTCATCTAGACAGACGCC 120
Qy 185 ATTACGCTGGCTTACTCTGATCTGTATTGGACTAGGACCGGACCTTGAAGAGC 244
Db 121 ATTACGCTGGCTTACTCTGATCTGTATTGGACTAGGACCGGACCTTGAAGAGC 180
Qy 245 CAATTACTCTCGGCTCCCGGAGAACCGCATTAGTAGGAGAAAGATGTGCTGTTC 304
Db 181 CAATTACTCTCGGCTCCCGGAGAACCGCATTAGTAGGAGAAAGATGTGCTGTTC 240
Qy 305 GGCCCACTCTCTCAATGACACTGGCAACTATACCTGATTTAAG 351
Db 241 GGCCCACTCTCTCAATGACACTGGCAACTATACCTGATTTAAG 287

RESULT 10
AA115283
ID AA115283 standard; DNA; 478 BP.
XX
AC AA115283;
XX
Xx 12-OCT-2001 (first entry)
Dc Probe #5216 for gene expression analysis in human cervical cell sample.
XX
Xx Probe: microarray; gene expression; cervical epithelial cell;
Xx cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
Xx (MOLE-) MOLECULAR DYNAMICS INC.
XX
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488901/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 5216; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SNP). The present sequence is one such probe. The SNPs are derived
CC from human HeLa cells. The SNPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 478 BP; 139 A; 105 C; 112 G; 122 T; 0 other;
Query Match 10.7%; Score 220; DB 22; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.8e-59;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 62 CAGAACGCTGCGATGACTGGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATG 121
DB 259 CAGAACGCTGCGATGACTGGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATG 318
QY 122 AGCCAGCTGCGATGACTGGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATG 181
DB 319 AGCCAGCTGCGATGACTGGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATG 378
QY 182 CCCATTGAGCTGGGCTTACTGATCTGTATTTGGACTAGGACGAGACCTTGAGG 241
DB 379 CCCATTGAGCTGGGCTTACTGATCTGTATTTGGACTAGGACGAGACCTTGAGG 438
QY 242 AGCCAACTTAATCTCGGCTCCCGAGAACCGCATTAGTAA 281
DB 439 AGCCAACTTAATCTCGGCTCCCGAGAACCGCATTAGTAA 478

ULT 11
36611
AAT36611 standard; DNA; 478 BP.

AC AAT36611;

DT 17-OCT-2001 (first entry)

DE Probe #5297 used to measure gene expression in human placenta sample.

XX Probe: microarray; human; placenta; antenatal diagnosis;

KM genetic disorder; ss.

XX Homo sapiens.

PN MO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001MO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

PT Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human placenta -

PS Claim 25; SEQ ID No 5297; 654bp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).

CC The present sequence is one such probe. The probes are useful for

CC producing a microarray for predicting, measuring and displaying gene

CC expression in samples derived from human placenta. The probes are useful

CC for antenatal diagnosis of human genetic disorders.

XX Sequence 478 BP; 139 A; 105 C; 112 G; 122 T; 0 other;

QY 62 CAGAACGCTGCGATGACTGGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATG 121
DB 259 CAGAACGCTGCGATGACTGGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATG 318

QY 122 AGCCAGCTGCGATGACTGGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATG 181
DB 319 AGCCAGCTGCGATGACTGGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATG 378
QY 182 CCCATTGAGCTGGGCTTACTGATCTGTATTTGGACTAGGACGAGACCTTGAGG 241
DB 379 CCCATTGAGCTGGGCTTACTGATCTGTATTTGGACTAGGACGAGACCTTGAGG 438
QY 242 AGCCAACTTAATCTCGGCTCCCGAGAACCGCATTAGTAA 281
DB 439 AGCCAACTTAATCTCGGCTCCCGAGAACCGCATTAGTAA 478

RESULT 12
ABN18246
ID ABN18246 standard; cDNA; 246 BP.

AC ABN18246;

DT 24-JUN-2002 (first entry)

DE Human ORFX polynucleotide sequence SEQ ID NO:4969.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

KM hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

KM degenerative disorder; osteoarthritis; neurodegenerative disorder;

KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KM hypertension; hypothyroidism; cholesterol ester storage disease;

KM immune deficiency; immune disorder; infectious disease;

KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;

XX myasthenia gravis; gene; ss.

OS Homo sapiens.

PN WO200192523-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001MO-US10836.

PR 30-MAY-2000; 2000US-206132P.

PR 29-AUG-2000; 2000US-228716P.

PR (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach MD;

XX WPI; 2002-106308/14.

DR P-PSDB; ABP02494.

PT Novel human polypeptides and polynucleotides useful for diagnosing,

PT preventing and treating cardiovascular disease, neurodegenerative,

PT hyperproliferative disorders and autoimmune disorders -

XX Disclosure; SEQ ID 4969; 1037bp; English.

PS The present invention describes substantially purified human proteins

CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

CC in the specification). ABN15762 to ABN27252 encode the human ORFX

CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for

CC treating or preventing a pathology associated with an ORFX-associated

CC disorder in humans, and in the manufacture of a medicament for treating a

CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide

CC sequences can be used in gene therapy. ORFX sequences can be used in the

CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,

CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,

CC osteoarthritis, neurodegenerative disorders, disorders related to organ

CC transplantation, cardiovascular diseases, diabetes mellitus, systemic

CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester

CC storage disease, various immune deficiencies and disorders, infectious

CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid

CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host

CC disease and autoimmune inflammatory eye disease. ORFX proteins are also

Qy	791	TTCCCTGTAAGGCTATATTAGTTTCTGTATGGAATCTGTGCATATAGAGTTGGTGACCA	850
Db	788	TCCCCTGTAAGGCAATCTCTGGGATTCAGTGAAGTCTGGGCCAATGATCTACTGGAAGA	847
Qy	851	TTGATGTGAAAAAAACCTGATGACATCACTATTGATGTCCCAATTAACGAATATATAGTC	910
Db	848	AAGGAGAAAAAGTTTATTTGAAGAACTGGCAGGTCACTTATGAAAGGTGAATTAAGGCTTC	907
Qy	911	ATTAGTAGAACAGATGATGAACAGAACTCAGATTTTGGAGCATCAAGAAAGTTACCTCTG	970
Db	908	TCAAAGAGCATCTTGGAGAAAAAGAAAGTTGAATTGGACACTCATTTTGACTCAGTTGTGG	967
Qy	971	AGGATTCACACCGAGCTATGTCGTCTGATGCTAGAAAGTCCAAAGCGGAAGTTGCCAAG	1030
Db	968	AAGCTGACCTGGCGAATTTAATACCTGCCTATGTTAAAAACGGAATGGAACGG-----AAAC	1021
Qy	1031	CAGCCAAAGTGTGAGCAGAAAGATGCCAGCTCCCAAGATATACAGTGAACCTGCTGTGGTT	1090
Db	1022	ATGCGACGTGTTTGTCTGCTGCTAATAAAGATTTAATCTATAAATGTAGCTTCGAGGGGGCC	1081
Qy	1091	TTGAGCAACAGTCTCTGCTAGTGTGATTTCTAATTGTTTACAAATGTTTACTGCTAG	1156
Db	1082	TGGGAGCAATCTTCTCTCTCTGTGACTGCTGTGGTCAATTTAACAAATGCTCAACATTTG	1141
Qy	1151	AGATGTGCTTATTTTACCGGGGCTCATTTTGGACAGATGAACCATTTTATGATGGAAG	1210
Db	1142	AATTGATGCTCTTCTTACAGGACAGACTTGGAGCTGATGAACATAATGATGACAAACAAAG	1201
Qy	1211	AGTATGATATTTATGATATCCATGACAAAG-----AATG	1243
Db	1202	AATATGATGCTTATCTCTCTTACCAAAATGAGCAAGATCACTTTAGCTGTGCAATC	1261
Qy	1244	CGGAAGAAAGAAATTTGTATTTACTGACCTCCGTGAGTTTGGAGAAATGAAATTTGAT	1303
Db	1262	CTGAAGAAAGAGCACTTTGCTCTTGAAGTATCTGCCAATGTCTCTGGAAAAACATAATGAT	1321
Qy	1304	ACAAGCTGTGATCTTTTGAACGAGACAGTCTGCTGGGGGAAATACAGTGAAGACATTT	1363
Db	1332	ATTAATCTTTTATCTCCAGAAAGAGACCTGATTTCCAAAGTGAACATPACATGGAAGATCTCA	1381
Qy	1364	TTGATTTTCAATTCAGAGAGACAGAAAGATGTTTGTCTGTGAGCCCTGACTATGTGACAG	1423
Db	1382	CAAGTATGTTTGAACAAAGCAGAAAGCTTATTTATGTGTAACTCCAGACTATATTCTCA	1441
Db	1424	AAAAAGCATCAGATCTGAGTTTAA	1452
Db	1442	GACCGGATGAGATATTTTGCAACTGAAA	1470
RESULT 14			
AADD21170			
ID	AADD21170 standard; DNA; 2061 BP.		
XX	AADD21170;		
XX	09-APR-2002 (first entry)		
XX	Human interleukin-1 receptor DNAX designation 8 (IL-1Rd8) DNA #2.		
DE	Human; morphogenesis; immune system; interleukin-1 DNAX designation 8;		
KM	IL-1Rd8 protein; therapy; immunological disorder; ds.		
KX	Homo sapiens.		
OS	Homo sapiens.		
XX	Key		
XX	Location/Qualifiers		
XX	1..2061		
XX	/*tag= a		
XX	/product= "Human IL-1Rd8 protein"		
XX	US6326472-B1.		
XX	04-DEC-2001		

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QY 491 ATGGATATTTCTTCAGTGTCAACCGACTATCACTTGATATGGGCTTTATAAA 550
DB 497 ATGACTTTAAAAAGCCGACGAGGCTGATGTTGTGTGTATAGAAATGACGCA 556
QY 551 TACAGATTTTAAATATGTAATACCCGAGGTAATGAATGAGTTTCTCATTTAA 610
DB 557 AATATGAGAAAGATTAATATACAGAAAGAAATGCTCTTGATTCAGAAATTCAG 616
QY 611 TTTCAATTAATGGAATTAACATGTGTTGTAATATCAATCAAGAAATGACGTTTC 670
DB 617 AAGAGATGAGGAAATTAACATGTAATTAATGAGGAAATCTGTAAAGGAA 676
QY 671 ATCTCAGAGACTCTGACTGTAAAGTATGAGCTCTCCAAAAATGCAAGTCCCTG 730
DB 677 CAATGAAATGAAGATTACAGCTTTACTACAGCAAGCCCTCCAGCCATGTCTCCA 736
QY 731 TGATCCATTCACCTAATGATCATGTGCTATGAGAAAGAACGAGAGAGCTACTCA 790
DB 737 TGGAGATACGCGCAAGTTATGATGTC-----AGCTGGGTAAAGCTCTGAACA 787
QY 791 TTCCTGTACGCTATTTTATGTTTCTGATGGAATTCCTGCAATGAGGTTGTGACCA 850
DB 788 TCCCTGCAAGCAATCTTGAGATTCAGTGAAGGTCCTGGGCCAATGATCTACTGATGA 847
QY 851 TTGATGAAAAAAACCTGATGATCATCTATTGATGTCACCATTAACGAAATTAATGTC 910
DB 848 AAGAGAAAAATTATTAAGAAATCGCAGGTCACATTAGAGAGGTAATAGGCTTC 907
QY 911 ATGTGAAACAGAGATGAACAAAGAACTCAGATTTGAGATCAAGAAATTAATCTG 970
DB 908 TCAAGAGCATCTTGAGAGAAAGAAAGATGATGATGCACTCATTTGATCAGTTGTG 967
QY 971 AGGATCTCAAGCGCAGCTATGTCTGATGCTAGAGTGCAGAAAGGAAATGCCAAG 1030
DB 968 AAGCTGACTGGGCAATTAATACCTGCATGTGAAACCGAAATGACGG-----AAG 1021
QY 1031 CAGCCAGGTGAAAGCAGAAAGTGCAGCTCCAGATACAGATGGAATCTGGCTTGTGCT 1090
DB 1022 ATGCAAGTGTGTGCTGCTGTAAGAAAGATTAATCTAATTAATGAGCTTGCAGGGGCC 1081
QY 1091 TTGAGCGCAGAGTCTCTAGTGTGATCTCATTTGTTTACCATGTTTACTGCTAG 1150
DB 1082 TGGAGCAATCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1141
QY 1151 AGATGCTCTATTTTACCGGCTCATTTTGAACAGATGAAACCAATTTAGATGAAAG 1210
DB 1142 AATTGATGCTCTCTCTACAGGAGACATTTGAGCTGATGAAATTAATGATGACAAAG 1201
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QY 1304 ACAAGCTGTGATCTTTGACCGAGACAGTCTGCTGAGGAGAAATATACGTGAGACGTT 1363
DB 1322 ATAAACTCTTCATCCAGAAAGAGACCTGATTCAGATGGAATCATATGAGATCTCA 1381
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QY 1424 AAAAGACATCAGCATCTGAGATTTAAA 1452
DB 1442 GACGGGATGAGATTTTTCGAATCTGGA 1470

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RESULT 15
ABA50826
ID ABA50826 standard; DNA; 169 BP.

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XX AC ABA50826;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #9521.
XX KW Human; microarray; single exon probe; gene expression; breast;
XX KW disease; cancer; ss.
XX OS Homo sapiens.
XX PN MO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00662.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR MPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes,
XX PT useful for measuring gene expression in sample derived from human
XX PT breast, comprises number of single exon nucleic acid probes
XX PS Claim 4; SEQ ID NO 9521; 327bp + sequence listing; English.

XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and BT 474 cells. The method involves contacting
XX CC the probes with a collection of detectably labelled nucleic acids
XX CC derived from mRNA of human breast, and then measuring the label
XX CC bound to each probe of the microarray. The probes are useful for
XX CC verifying the expression of regions of genomic DNA predicted to
XX CC encode proteins. They are useful for gene discovery, and for
XX CC determining predisposition and/or prognosing breast disease. Gene
XX CC expression analysis is useful for assessing the toxicity of chemical
XX CC agents on cells. The microarray of this invention presents a far greater
XX CC diversity of probes for measuring gene expression, with far less bias
XX CC than expressed sequence tag microarrays. The method is suitable for
XX CC rapid prediction of functional information from genomic sequence. The
XX CC present sequence is a single exon nucleic acid probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO.int/ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 169 BP; 62 A; 29 C; 44 G; 34 T; 0 other;
Best local Match 7.2%; Score 149; DB 22; Length 169;
Best Local Similarity 100.0%; Pred. No. 6.7e-37;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 903 TATATGCTATAGTAGAAGCAGAGATGAACAAAGAACTCAGATTTTGAAGCATCAAGAAAT 962
DB 1 TATATGCTATAGTAGAAGCAGAGATGAACAAAGAACTCAGATTTTGAAGCATCAAGAAAT 60
QY 963 TACCTGAGAGATCTCAAGCGCAGCTATGCTGCTATAGAGGCCAAGGCGGAAT 1022
DB 61 TACCTGAGAGATCTCAAGCGCAGCTATGCTGCTATAGAGGCCAAGGCGGAAT 120
QY 1023 TGCCAAAGCAGCCAGGTGAAGCAAGAAAG 1051

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Thu May 1 09:36:46 2003

us-10-061-727-1.rng

Page 15

Db 121 TGCCAAAGCAGCCAAAGGTGAAGCAGAAAG 149

Search completed: April 30, 2003, 08:04:12
Job time : 328 secs

Query Match	51.7%;	Score 1067.4;	DB 4;	length 3355;
Best Local Similarity	78.9%;	Pred. No. 0;		
Matches 1298;	Conservative 0;	Mismatches 341;	Indels 6;	Gaps 2

1	ATGCACTTCTGGGTGTGTAGTAGTCTCTACTTTATGGAATTCGCAAGATGAGCC	60
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Qy	61 TCAGAACCTCGCATGACTGGGAGCTAGACACCAATGAGCAAAATCCAGTGTGAAGAT	120
Db	195 TCGAGCCCTGTGATGACTGGGGACTAGATTCAGATGCAAAATCCAGTGTGAAGAT	255
Qy	121 GAGCAGCTGCATCAAGTGGCCACTCTTGAACACTCTGGAATTTCACTAAGACA	180
Db	255 GAGCGGGCTGAAATCAAGTGGCCCTCTTGAACACTCTGGAAGTTCAACTAAGACA	315
Qy	181 GCCCATTCAGCTGGCCTTACTCTGATCTGTATTTGACTAGGACGAGACCGGACTTGGAG	240
Db	315 GCCCATTCCTGTGGCTTAACTCTGATCTGTATTCGACGACGAGACCGGACTTGGAG	375
Qy	241 GAGCCAAATTAATCTTCGCTCTCCCGAGAACCGCAATTAAGAGAAAGATGTGCTGTGG	300
Db	375 GAGCCCAATTAATCTTCGCTCTCCAGAGATGCAATCAATTAAGAGAAAGATGTGCTGTGG	435
Qy	301 TTCGGGCCCCCTCTCAATGACACTGGGCAACTATACCTGTCAGTTTAAGAAACAATCA	360
Db	435 TTCGGGCCCCCTCTCTCAATGACACGGGCAATTAACCTGTCAGTTTAAGAGAAACA	495
Qy	361 TATTGCAAGCAAAAGTTGCAATTTCCCTTGGAGTTGTTCAAAAAGACCTGTTCAATTC	420
Db	495 TATTGCAAGCAAAAGTTGCAATTTCCCTGGAAGTTGTTCAAAAAGACCTGTTCAATTC	555
Qy	421 CCCATGAAATCTCCAGTGCATAAACTGTATATAGAAATGSCATTCAGAGATCACTTGT	480
Dv	555 GGCATGAGATTTCCAGTGCACAAATGTATATTAACAATGSCATTCATTAAGATCACATGT	615
Qy	481 CCAATGATGATGATATTTTCCCTTCAGATGCAAAACGACTATACCTGGTATATAGGC	540
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Qy	601 AATGCTTAATTTGAAATTAATGAGAAATTAACAATGTGTGTTACTATATCCAGAAATGCA	660
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Qy	661 CGTAGTTCATCTCACACAGACTCTGACTGTAAAGGTAGAGGCTCCCAAAAAATGCA	720
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Qy	721 GTGCCCCCTGTGATCAATTCACCTAATGATCATGTGTTCTATGAGAAAGAACAGAGAG	780
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1 RESULT 3
2 US-09-173-151A-3
3 ; Sequence 3, Application US/09173151A
4 ; Patent No. 6326472
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Timans, Jacqueline C.
9 ;
10 ; APPLICANT: Debets, Johannes Eduard Maria
11 ;
12 ; APPLICANT: Antonius
13 ;
14 ; APPLICANT: Sana, Theodore R.
15 ;
16 ; APPLICANT: Bazan, J. Fernando
17 ;
18 ; APPLICANT: Kastelein, Robert A.
19 ;
20 ; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
21 ;
22 ; NUMBER OF SEQUENCES: 36
23 ;
24 ; CORRESPONDENCE ADDRESS:
25 ;
26 ; ADDRESSEE: DNAX Research Institute
27 ;
28 ; STREET: 901 California Avenue
29 ;
30 ;

```


OY 1364 TTGATTTCAGAGACAGAGATATTGTTCTGAGCCCTGACTATGACAG 1423
DB 1382 CAAGATATCTGGAACAAGACACTATATCTGCTAACTCCAGACTATATCTCA 1441
OY 1424 AAAAGAGATCGACATGCTGAGCTTTAA 1452
DB 1442 GACGGGATGAGATATTTTGAAGCTGAA 1470

RESULT 4

US-09-173-151A-34
Sequence 34, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2004

US-09-173-151A-34

Query Match 7.0%; Score 144.4; DB 4; Length 2537;
Best Local Similarity 46.2%; Pred. No. 1.9e-36;
Matches 640; Conservative 0; Mismatches 701; Indels 45; Gaps 3;

OY 94 ATGAGCAATTCAGAGTCTTGAAGATGAGCCAGCTGCATCACTAGTCCACTTTTGA 153
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OY 154 CACTTCTGAAATTCACATCAAGACAGCCCATTCAGCTGCGCTTATCTGTGTTAT 213
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DB 148 AAAGTTCTGCTCTGAGACTTGAAGAGCCAAATAGCT-----TTAGGAAGTGA 201
OY 274 ATTAGTAAGAGAAAGATGTGTGTGTGTCGCGCCACTCTCTCAATGACACTGGCAAC 333
DB 202 ATGACCAAGAGAAAGATCCATTTGTTCCGCAATTTGCTACAGGAGAGTGTCTC 261
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OY 454 GAATATGACATTCAGAGATCACTGTCCAAATGATATATTTTCTCCAGTGC 513
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OY 514 AAACGACTATCACTGTGTATATGAGCTGTATTAATTAATTAATTAATTAATTA 573
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OY 574 CCGGAGGTATGAATCTGATGTTCTCATGCTTAAATTTGAAATTAATTAATTA 633
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DB 730 GGTACAGCGAGATGTATCTCTTTAATTTAATGATGAGAAATTAATTAATTAATTA 789
OY 874 ATCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 933
DB 790 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 849
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OY 994 TGTATGCTAGAGAGCAAGGAGAGGAGGTGCAAGAGAGCAAGGAGAGAGAGAG 1053
DB 910 TACTCTGTATGTTGAAATGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 969
OY 1054 CCAGCTCAAGATACAGAGTGAAGTGTGCTTGTGTTTGAAGCCAGTCTGCTAGTG 1113
DB 970 CGAGAGCTATATGATACAGAGTGAAGTGTGCTGAGAGCTTGTGTGATATCTGTGCTG 1029

Db 295 CACTACCTGAGGCAAGAGAGGATTTCTACCTGTGTTTAAAGAACTCAACATAT 354
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 Db 415 AGCAGATCCGCTATTTAGAAAATTCAGAGTCACTAAAAGAAAGAGATCTCTGTCCA 474
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 Db 535 AAGCAAAAATGTGAGAGATATATATATAGAAAGAAATGCTCTTGTGATCAAGAA 594
 Qy 604 GCCTTAATTTCAATATATGAAATATACATGTGTGTTCATATCCAGAAATGACGT 663
 Db 595 GTTCAAGAGAGATGAGGAAATATACATGTGATTAATATGAGGAAATCTGTGA 654
 Qy 664 ACCTTATATCTACAGAGATCTGACTGTAAAGTATAGGCTCTCCAAAATGCACTG 723
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 Db 766 CTGAACATCCCTGTCAAGATCTTGTGATTCAGTGAAGATCTGGCCATATATCTAC 825
 Qy 844 TGAACATGTATGAGAAAAAAGCTGATGATCACTATGATGTACATTAACGAAAT 903
 Db 826 TGAATGAAGAGAGAAAGTTATATGAAAGATCTGACAGTCACTTGAAGAGGATA 885
 Qy 904 ATAGTATGTATGAACAGAAATGAAAGAACTCAGATTTTGACATCAAGAAAT 963
 Db 886 AGCTTCTCAAGAGATCTTGAAGAAAGAAATGAAATGGAATCTTGTGATCTCA 945
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 Qy 1204 GGAAGAGATGATATATATATATCTATGCAAG-----1239
 Db 1180 AACAGAGATATATATGCTATCTCTTACACAAAGTGAACCAAGATCTTATAGATGT 1239
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 Db 1300 TATGATATTAATCTTCTATCTCCAGAAAGAGCTGATTCAGAGTGAAGTGCATACATG 1359
 Qy 1354 GAAGCAGTTTTTGAATTCATTCAGAGAGAGAGATGTGTGTGTGTGTGTGTGTGTGTGT 1413

Db 1360 GAAGATCTCAAGATATGTGTAACAAGAGAGAGCTTATATCTGCTACTCCAGAC 1419
 Qy 1414 TATGTGACAGAAAAAGAGATCAGAGATGAGAGTTTAA 1452
 Db 1420 TATATCTCAGACGGGAGATGAGATATTTTGAAGTGA 1458

RESULT 6
 US-08-604-333-1
 ; Sequence 1, Application US/08604333
 ; Patent No. 5776731
 ; GENERAL INFORMATION:
 ; APPLICANT: Parnet, Patricia et al.
 ; TITLE OF INVENTION: Receptor Designated 2P1
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/604,333
 ; FILING DATE: 21-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Anderson, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2619
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ. ID NO. 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1626 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; IMMEDIATE SOURCE:
 ; CLONE: hu2F1
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1626
 ; FEATURE:
 ; NAME/KEY: mat peptide
 ; LOCATION: 58..1623
 ; FEATURE:
 ; NAME/KEY: sig peptide
 ; LOCATION: 1..57
 ; US-08-604-333-1
 Query Match 4.3%; Score 89.6; DB 1; Length 1626;
 Best Local Similarity 46.3%; Pred. No. 1, 1e-18;
 Matches 391; Conservative 0; Mismatches 423; Indels 24; Gaps 2;

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QY 784 CTACTCATTCCTGTAAGGCTATATTTAGTTTCTGATGATTCGCAATGAGTTTG 843
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QY 904 ATAAGTCATAGTGAACAGAAAGATGAACAGAACTCAGATTTTGAGCATCAAGAAAGT 963
Db 823 AATGCGATCTCTCAAAAGATGATGAGAAATATGTTGTAAGCAATCTAAATGTT 882
QY 964 ACCTGAGATCTCAAGCCGACTATGTCTGTCATCTGAACTGCAAGGCAAGTT 1023
Db 883 TTATATATTTGCACTGTGGCAGAGGAGGACAGACACCAAAAGCTTCACTTGTG 942
QY 1024 GCCAAGCAGCCAGAGTGAAGAGAAAGTGCAGCTCCAGATACAGATGAGAACTGGCT 1083
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QY 1144 TGGCTAGAGATGCTCTATTTTACCGGGCTCATTTTGGAAACAGATGAAACCATTTTATGAT 1203
Db 1063 T-----TGGTCTATTTTATAGACATTTAAGAGAAAGATGAAACATTAACGAT 1113
QY 1204 GGAAGAGATGATATTTATTTATGATCTTATGCA-----GGAATGCGAA 1248
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QY 1249 GAAGAGATTTGATATCTGACCTCCGATGAGTTTGGAGAAATTTGGATPACAG 1308
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Db 1234 TTATGATATTTGAAGAGATGATGTGCTGAGAGAGCTGTGTTGATGAATCACTCA 1293
QY 1369 TTCTATGAGAGAGAGAGATGATTTGTTTCTGAGCCCTGATGATGACAGAAAG 1428
Db 1294 CTGATGAGAGAAAGCCAGAGCTATGATCTTCTAAGTAAAGTTATATGTCTTAATGAG 1353
QY 1429 AGCA 1432
Db 1354 GTCA 1357

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/110,618
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,333
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hu2P1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1626
; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: 58..1623
; FEATURE:
; NAME/KEY: sig.peptide
; LOCATION: 1..57
; US-09-110-618-1
;
Query Match 4.3%; Score 89.6; DB 3; Length 1626;
Best Local Similarity 46.3%; Pred. No. 1.1e-18;
Matches 391; Conservative 0; Mismatches 429; Indels 24; Gaps 2;
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QY 604 GCCTTAATTCATTAATGAGAAATATACATGTTGTTTACATATCCAGAAATGACGT 663
Db 523 GCCGATTTGAAGATCAGGGATATTAATCTCTGCTGATTTCTTCAATTAATGAAA 582
QY 664 AGTTTCATCTCAGCAGACTGTGACTGTAAAGGTAGAGCTCTCCAAAATGCACTG 723
Db 583 CTATTTATATACCAAAACCTTCAATATTAACAATAGTGAAGATCGAGTAATATAGTT 642
QY 724 CCCCCTGTGATTCATTAACCTTAATGATCATGTGCTCTATGAGAAAGAACAGAGAGAG 783
Db 643 CCGGTTCTTTTGGACCAAGGCTTAACCATGTTGCACTGAGAAATTAAGAAAAAGTAAAG 702
QY 784 CTACTCATTCCTGTAAGGCTATATTTAGTTTCTGATGATTCGCAATGAGTTTG 843
Db 703 CTCAACTGCTCTGCTTGTGTAATGAGAGATGTAAATTAATGATGTTGGGAGAA 762
QY 844 TGAACCATGATGAGAAAAAACCCTGATGACATCTATGATGTCACCATTAAGAAAGT 903
Db 763 AATGATCGGATCTATATATACATGAGAGAAAGAAATGAAATTAATGATCCAGAAAGC 822
QY 904 ATAAGTCATAGTGAACAGAAAGATGAACAGAACTCAGATTTTGGACATCAAGAAAGT 963
Db 823 AATGCGATCTCTCAAAAGATGATGAGAAATATGTTGTAAGCAATCTAAATGTT 882
QY 964 ACCTGAGATCTCAAGCCGACTATGTCTGTCATCTGAACTGCAAGGCAAGGAGTT 1023
Db 883 TTATATATTTGCACTGTGGCAGAGGAGGACAGACACCAAAAGCTTCACTTGTG 942
QY 1024 GCCAAGCAGCCAGAGTGAAGAGAAAGTGCAGCTCCAGATACAGATGAGAACTGGCT 1083
Db 943 AGAAAGCAGACATGGCTGATATCCAGGCCACGCTTTCACAAAGAGAAATGATATAGCT 1002

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OY 1429 AGCA 1432
Db 1354 GTCA 1357

RESULT 9

US-09-173-151A-19
Sequence 19, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1458
US-09-173-151A-19

Query Match 4.3%; Score 88.6; DB 4; Length 1991;
Best Local Similarity 52.8%; Pred. No. 2,8e-18;

Matches 236; Conservative 0; Mismatches 184; Indels 27; Gaps 1;

OY 1033 GCCAAGGTGAAGAGAAAGTCCAGCTCCAGATTAACAAGTGAACCTGGCTTGTTT 1092
||| |
Db 403 GCCAGCGTTCCTCTTCAATAACGAGAGCTAATGTACACAGTGAACCTGAGGCTT 462
||| |
OY 1093 GGAAGCCAGTCCGCTAGTGGTGAATTCATTTGTTTACCATGTTTACTGGTAGAG 1152
||| |
Db 463 GGTGCTATCTCTTGGCTGCTTGTATGTGTTGGTACCATCTTACAGAGTTTCAAGATGGA 522
||| |
OY 1153 ATGCTCTATTTTAAACGGGCTCATTTTGAACAGATGAAACATTTAGATGAAAGAG 1212
||| |
Db 523 ATCATGCTCTTTACAGAGATCAATTTTGGAGCTGAAGAGCTGCATGAGACAATTAAGAT 582
||| |
OY 1213 TATGATTTTATGTATCT-----ATGCAAGGATGCG 1245
||| |
Db 583 TATGATGCTATATCTATCATACACCAAGTGAATCTGACCAAGTGAATCAAGAGACTGGG 642
||| |
OY 1246 GAAGAAGAGAAATTTGTATTACTGACCCCTCGAGAGTTTGGAGAAATTTGATAC 1305
||| |
Db 643 GAAGAGAAAGCTTTTGCCCTTGAATCTTACCTGATATGCTTGAAGATTTATGATAT 702
||| |
OY 1306 AAGCTGTGATCTTTTGAACCGAGACAGTCTGCGGGGAATACAGTGAAGCAATTTT 1365
||| |
Db 703 AAGTTGTTTATACAGATAGAGATTTAATCCAACTGGAACATATGAAGATGCGCA 762
||| |
OY 1366 GATTTCAATCAGAGAGACAGAGATGTTGTTCTGAGCCCTGACTATGACAGAA 1425
||| |
Db 763 AGATGTGATATCAAGAGCAAGCAGCTGATTTGTATGATGACCCCAATTAATGATGAGA 822
||| |
OY 1426 AAGGATCAGATGCTGAGGTTTAA 1452
||| |
Db 823 AGGGCTGAGAGATCTTTGAGCTGAA 849
||| |

RESULT 10

US-08-996-338-1
Sequence 1, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takamori
APPLICANT: KURIMOTO, Mutsashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3

RESULT 12
 US-08-996-338-2
 : Sequence 2, Application US/08996338
 : Patent No. 6087116
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: TOPRICE, Kakui
 : APPLICANT: OKURA, Takaochi
 : APPLICANT: KUMIMOTO, Mutsaht
 : TITLE OF INVENTION: POLYPEPTIDES
 :
 : NUMBER OF SEQUENCES: 37
 :
 : CORRESPONDENCE ADDRESS:

```

ADDRESS: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1557 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: mat peptide
LOCATION: 1..1557
IDENTIFICATION METHOD: S
US-08-996-338-2

Query Match 3.5%; Score 73; DB 3; Length 1557;
Best Local Similarity 54.2%; Pred. 2.9e-13;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 1182 AACGATGAAACCTTTAGATGAAAGAGATGATATTATGTATCTTATGCAAGAA 1241
      |||||
Db 1044 AACGATGATGAAACATATGATGCTTTGTGTCTTACCTGAAAGTGTATCTCGAATA 1103
      |||||
QY 1242 TGGCGAAGAGAAATTTGTATTAAGTACCCCTCGTGAGTTTGGAGATGAATTGG 1301
      |||||
Db 1104 TAAAGAAAGATATCTTTGCTGTGAGACCTTACCCAGAGTCTCGAGAAACAGTTGG 1163
      |||||
QY 1302 ATACAGCTGTGATCTTTTGAACCGAGACAGTCTGCTGGGGGAAATATACGTGAAGCAGT 1361
      |||||
Db 1164 GTATTAAGTATTAATTTGAAAGAGATGTGTGCTCGGCGAGAGCTGTTCGAGAGAT 1223
      |||||
QY 1362 TTTTGAATTTATTAGAGAAACAGAGATGATTTGTTTGTAGACCTGACTATGTGAC 1421
      |||||
Db 1224 CCATTCACGTATTAAGAAAGCCGAGAGCTATATCATGTTCTCGACGAGATTAAGTAC 1283
      |||||
QY 1422 AGAAAGAGCATGACATGCTGAGTTTAAGT 1454
      |||||
Db 1284 TAACGAGCCGAGCGTGAAGCTCGAGAGTGAAT 1316
      |||||

RESULT 13
US-08-604-333-3
; Sequence 3, Application US/08604333.
; Patent No. 5776731
; GENERAL INFORMATION:

```

APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: mu2F1
FEATURE:
NAME/KEY: CDS
LOCATION: 381..1994
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 435..1991
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 381..434
-08-604-333-3
Query Match 3.5%; Score 73; DB 1; Length 2830;
Best Local Similarity 54.2%; Pred. No. 4.4e-13;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
Qy 1182 AACAGATGAACCATTTAGATGGAAGATATGATATTTATGATCTATGCAAGAA 1241
Db 1478 AACAGATGTAACCATATGATGCTTTGTCTTACCTGAAGATGATCTGAGAA 1537
Qy 1242 TCGCGAAGAAAGATTTGTATTACTGACCCCTCGGAGTTTGGAGAAATTTGG 1301
Db 1538 TAAAGAGAGTATATCTTTCTGAGAGCTTACCCAGGCTCTGAGAAACAGTTTGG 1597
Qy 1302 ATCAAGCTGTGATCTTTGACGAGACAGTCTGCGGGGAATACAGTGAAGCAGT 1361
Db 1598 GTATTAAGTTATGATATTTGAAAGATGTGTGCTGCGGAGCTGTGTCGAGAGAT 1657
Qy 1362 TTTTGAATTCATTCAGAGAGAGATGATTTGTCTGAGCCCTGACTATGTGAC 1421
Db 1658 CCAATTAATGATAGAGAAAGCGGAGGCTAATCATGTTCTGACGAGATTACCTGAC 1717
Qy 1422 AGAAAAGCATCAGCATGCTGAGATTAACT 1454
Db 1718 TAAAGAGCCAGGCGTGTGAGCTGAGAGTGA 1750

RESULT 14
US-09-110-618-3
Sequence 3, Application US/09110618
Patent No. 6090918
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/110,618
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: mu2F1
FEATURE:
NAME/KEY: CDS
LOCATION: 381..1994
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 435..1991
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 381..434
US-09-110-618-3
Query Match 3.5%; Score 73; DB 3; Length 2830;
Best Local Similarity 54.2%; Pred. No. 4.4e-13;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
Qy 1182 AACAGATGAACCATTTAGATGGAAGATGATATTTATGATCTATGCAAGAA 1241
Db 1478 AACAGATGTAACCATATGATGCTTTGTCTTACCTGAAGATGATCTGAGAA 1537
Qy 1242 TCGCGAAGAAAGATTTGTATTACTGACCCCTCGGAGTTTGGAGAAATTTGG 1301
Db 1538 TAAAGAGAGTATATCTTTCTGAGAGCTTACCCAGGCTCTGAGAAACAGTTTGG 1597
Qy 1302 ATCAAGCTGTGATCTTTGACGAGACAGTCTGCGGGGAATACAGTGAAGCAGT 1361
Db 1598 GTATTAAGTTATGATATTTGAAAGATGTGTGCTGCGGAGCTGTGTCGAGAGAT 1657

OY 1362 TTTGATTTCATTCAGAGAGAGAGATGTTGTTCTGAGCCCTGACTATGTAC 1421
 DB 1658 CCATTCACTGATGAGAAAGCCGAGGCTATTCATCGTTCTCAGCCAGAGTTACTGTAC 1717
 OY 1422 AGAAAAGACATCAGATGCTGAGGTTAACT 1454
 DB 1718 TAACGAGCCAGCGCTGAGCTCAGAGTGAGCT 1750

RESULT 15

US-09-578-178-3
 ; Sequence 3, Application US/09578178
 ; Patent No. 6451760

; GENERAL INFORMATION:
 ; APPLICANT: Parinet, Patricia et al.
 ; TITLE OF INVENTION: Receptor Designated 2F1
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kathryn A. Anderson, Immumex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/578,178

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/110,618

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2619

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:

LENGTH: 2830 base pairs

TYPE: 'nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHEICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:
 CLONE: mu2F1

FEATURE:
 NAME/KEY: CDS

LOCATION: 381..1994

FEATURE:
 NAME/KEY: mat_peptide

LOCATION: 435..1991

FEATURE:
 NAME/KEY: sig_peptide

LOCATION: 381..434

US-09-578-178-3

Query Match

Best Local Similarity 54.2%; Score 73; DB 4; Length 2830;

Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

OY 1182 AACAGATGAACATTTTGAAGAAAGATGATTTATGATTCATGCAAGAA 1241

DB 1478 AACAGATGTAACATATGATGCTTTGTGTCTTACTGAAAGATGTCATCTGAGAA 1537
 OY 1242 TCGGAGAGAGAGATTTGATTACTGACCCCTCGTGAGTTTGGAGATGAATTTGG 1301
 DB 1538 TAAAGAGATGATTTCTTTGCTGTGAGACGTTACCGAGGCTCTGAGAGAAACAGTTGG 1597
 OY 1302 ATCAAGCTGTGATCTTTGACCGAGACGTCGCTGAGGAGAAATACATGAGAGAGT 1361
 DB 1598 GTATAGTTATGATATTTGAAAGATGTGTGCTGCGAGCTGTTGTGAGAGAGAT 1657
 OY 1362 TTTGATTTCATTCAGAGAGAGAGATGTTGTTCTGAGCCCTGACTATGTAC 1421
 DB 1658 CCATTCACTGATGAGAAAGCCGAGGCTATTCATCGTTCTCAGCCAGAGTTACTGTAC 1717
 OY 1422 AGAAAAGACATCAGATGCTGAGGTTAACT 1454
 DB 1718 TAACGAGCCAGCGCTGAGCTCAGAGTGAGCT 1750

Search completed: April 30, 2003, 09:41:32
 Job time : 76 secs


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Db 181 GCCATTACAGTGGCCTTACTGATCTGATCTGATTTAGATAGGAGACCGGGACCTTGAG 240
Qy 241 GAGCCAAATTAATCTCCGCTCTCCGAGAACCGCAATTAGTAAGAGAAAGATGCTGTGG 300
Db 241 GAGCCAAATTAATCTCCGCTCTCCGAGAACCGCAATTAGTAAGAGAAAGATGCTGTGG 300
Qy 301 TTCCGGCCACTCTCTCAAGACATGGGCAATTAACCTGCAATGTTAAAGAACTACA 360
Db 301 TTCCGGCCACTCTCTCAAGACATGGGCAATTAACCTGCAATGTTAAAGAACTACA 360
Qy 361 TATTGACAGCAAGTGTGATTTCCCTGGAAGTGTTCAAAAGACAGCTGTTCAATTC 420
Db 361 TATTGACAGCAAGTGTGATTTCCCTGGAAGTGTTCAAAAGACAGCTGTTCAATTC 420
Qy 421 CCCATGAACTCCGATGATTAACCTGTAATAGAAATATGSCATTCCAGAGATCACTTGT 480
Db 421 CCCATGAACTCCGATGATTAACCTGTAATAGAAATATGSCATTCCAGAGATCACTTGT 480
Qy 481 CCAAAATGATGATGATTTTCTCCAGTGTCAACCGATATCACTTGTATATGAGC 540
Db 481 CCAAAATGATGATGATTTTCTCCAGTGTCAACCGATATCACTTGTATATGAGC 540
Qy 541 TGTATATTAATTAAGAAATTTTATATATATATATATATATATATATATATATATAT 600
Db 541 TGTATATTAATTAAGAAATTTTATATATATATATATATATATATATATATATATAT 600
Qy 601 ATTGCTTAATTTCAAAATATATGAAATTTACATGTTGTTACATATCCAGAAATGGA 660
Db 601 ATTGCTTAATTTCAAAATATATGAAATTTACATGTTGTTACATATCCAGAAATGGA 660
Qy 661 CATTACGTTTATCTACAGAGATCTGATCTGTAAGATGATGCTCTCCAAAATGCA 720
Db 661 CATTACGTTTATCTACAGAGATCTGATCTGTAAGATGATGCTCTCCAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCTATCACTTAATGATGATGCTATGAGAAAGAACAGAGAG 780
Db 721 GTGCCCCCTGTGATCTATCACTTAATGATGATGCTATGAGAAAGAACAGAGAG 780
Qy 781 GAGTACTATCTCCCTGATGAGGTCTATTTAGTTTCTGATGATTTCTGCAATGAGGT 840
Db 781 GAGTACTATCTCCCTGATGAGGTCTATTTAGTTTCTGATGATTTCTGCAATGAGGT 840
Qy 841 TGTGTGACATTTGATGAGAAAGAACTGATGATCACTATGATGATGATGATGATGAT 900
Db 841 TGTGTGACATTTGATGAGAAAGAACTGATGATCACTATGATGATGATGATGATGAT 900
Qy 901 AGTATAGTCAATGATGAGAAAGAACTGATGATCACTATGATGATGATGATGATGAT 960
Db 901 AGTATAGTCAATGATGAGAAAGAACTGATGATCACTATGATGATGATGATGATGAT 960
Qy 961 GTTACTCTGAGATCTCAACGAGCTATGCTGCTGCTAGAGAGGCGAA 1020
Db 961 GTTACTCTGAGATCTCAACGAGCTATGCTGCTGCTAGAGAGGCGAA 1020
Qy 1021 GTTGGCAAAGAGAGCAAGTGAAGAAAGTGCAGCTCCAAAGTACAGTGAATG 1080
Db 1021 GTTGGCAAAGAGAGCAAGTGAAGAAAGTGCAGCTCCAAAGTACAGTGAATG 1080
Qy 1081 GCTTGTGTTTGGAGCAGTCTCTGATGATGATTTCAATGTTGTTTACATGTT 1140
Db 1081 GCTTGTGTTTGGAGCAGTCTCTGATGATGATTTCAATGTTGTTTACATGTT 1140
Qy 1141 TACTGGCTAGAGATGCTCTATTTTACCGGCTCATTTTGAACAGATGAACCAATTTA 1200
Db 1141 TACTGGCTAGAGATGCTCTATTTTACCGGCTCATTTTGAACAGATGAACCAATTTA 1200
Qy 1201 GATGGAAGAGATGATGATTTATGATATCTATGCAAGGAATGGGAGAGAGAGAAATTT 1260
Db 1201 GATGGAAGAGATGATGATTTATGATATCTATGCAAGGAATGGGAGAGAGAGAAATTT 1260
Qy 1261 GTATTAAGACCTCTCCGTGAGTTTGGAGATGAATTTGGATACAGCTGTGATCTTT 1320
Db 1261 GTATTAAGACCTCTCCGTGAGTTTGGAGATGAATTTGGATACAGCTGTGATCTTT 1320

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Db 1261 GTTATACGACCTCCGTGAGTTTGGAGATGAATTTGGATACAGCTGTGATCTTT 1320
Qy 1321 GACCGAGACAGTCTGCTGGGGGAAATATACAGTGAAGCACTTTTATATTCATTCAGAG 1380
Db 1321 GACCGAGACAGTCTGCTGGGGGAAATATATACAGTGAAGCACTTTTATATTCAGAG 1380
Qy 1381 AGCAGAGATGATGATTTGTTCTGAGCCCTGATCTATGATGACAGAAAGACATCAGATG 1440
Db 1381 AGCAGAGATGATGATTTGTTCTGAGCCCTGATCTATGATGACAGAAAGACATCAGATG 1440
Qy 1441 CTGAGATTAATACGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Db 1441 CTGAGATTAATACGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Qy 1498 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
Db 1498 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
Qy 1558 ---TCTTTGTGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1614
Db 1558 ---TCTTTGTGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1614
Qy 1615 GCTTTGGGTTGCTCTCTCTCTCTGAGAGAGTGTGATGATGATGATGATGATGATGATGAT 1674
Db 1615 GCTTTGGGTTGCTCTCTCTCTCTGAGAGAGTGTGATGATGATGATGATGATGATGATGAT 1674
Qy 1675 TGTCTTTCCAGTTC 1688
Db 1675 TGTCTTTCCAGTTC 1688
Qy 1681 GGCCTCTCGTATTC 1694
Db 1681 GGCCTCTCGTATTC 1694

RESULT 2
US-10-215-211-5
; Sequence 5, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1077)
; OTHER INFORMATION:
US-10-215-211-5

Query Match 52.1%; Score 1075.4; DB 9; Length 1077;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1076; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 16315
LENGTH: 478
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008249.14
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
09-864-761-16315

Query Match 10.7%; Score 220; DB 10; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 CAGACGCTGCGATGACTGCGGACACTAGACACCAATGAGCAATCCAGTGTGGAAGATG 121
Db 259 CAGACGCTGCGATGACTGCGGACACTAGACACCAATGAGCAATCCAGTGTGGAAGATG 318
Qy 122 AGCAGCTGCGATGACTGCGGACACTGTTGAACACTTCTGAAATTCACATACAGCAG 181
Db 319 AGCAGCTGCGATGACTGCGGACACTGTTGAACACTTCTGAAATTCACATACAGCAG 378
Qy 182 CCATTCAGTGGCTTCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 241
Db 379 CCATTCAGTGGCTTCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 438
Qy 242 AGCATTAACTTCGCGCTCCCGAGAACGCGATTAGTAA 281
Db 439 AGCATTAACTTCGCGCTCCCGAGAACGCGATTAGTAA 478

RESULT 6
US-10-011-548-3
Sequence 3, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Debets, Johannes Edward Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.

TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151

Qy 11 TGTGCTGTGATGATGATCTCTACTTTATGGAATCTTGCAAGATGCTCAGAAAGCT 70
Db 32 TGTGCTGTGATGATGATCTCTACTTTATGGAATCTTGCAAGATGCTCAGAAAGCT 91
Qy 71 GCGATGATGCGGAGCTAGACACCATGAGGCAATCCAGTGTGGAAGATGAGCCAGCTC 130
Db 92 GCGATGATGCGGAGCTAGACACCATGAGGCAATCCAGTGTGGAAGATGAGCCAGCTC 148
Qy 131 GCATCAAGTCCGACCTCTTGAACACTTCTGAAATTCACATACAGCAGCCATTAG 190
Db 149 GAGTGAATGTGCTTCTTCTACATATATTCGTACCAACTATACAGCAGCCAGGAGCA 208
Qy 191 CTGGCTTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 250
Db 209 CTGGCTTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 262
Qy 251 ACTTCGCTCCCGAGAACCGCATTAAGAGAGAAATGCTGTGCTCCGCGCA 310
Db 263 TCTTT-----TCAGAGTCAAGATGAGCAAGAGAGAAATTCATATGCTTCACTAG 316
Qy 311 CTCTCTCAATGACACTGCAATTAATCTGCACTGTTAAGAAACATCAATATGAGCA 370
Db 317 CTGAGGACAAAGACAGTGAATCTACACTGTGTTTAAAGAACTCAATATATGATGA 376
Qy 371 AAGTGAATTCCTGGAAGTGTCAAAAAGACAGCTGTTCAATCCCCCATGAAC 430
Db 377 AAGTGAATTCCTGGAAGTGTCAAAAAGACAGCTGTTCAATCCCCCATGAAC 436
Qy 431 TCCAGTCAATAACTGATATATGATATGCAATTCAGAGATCACTGTCCAAATGAG 490
Db 437 TCCAGTCAATAACTGATATATGATATGCAATTCAGAGATCACTGTCCAAATGAG 496
Qy 491 ATGATATATTTCTTCCAGTGTCAAAACGACATATCACTGTTGATATGAGCTGTTAATAA 550
Db 497 ATGATATATTTCTTCCAGTGTCAAAACGACATATCACTGTTGATATGAGCTGTTAATAA 556

Qy 551 TACAGATTTTAAATATGTAATACCCGAGGTATGACCTTACCTTACCTTAA 610
Db 557 AAATGTGAGAAAGCATATATATAGAAAGAAATGCTCTTGTATCCAAAGATTCAG 616
Qy 611 TTTCAATATATGAAATTTACACATGTGTTTACATATCCAGAAATGACGTACGTTTC 670
Db 617 AAGAAATGAGGAAATTTACACATGTGAACTTAATATGAAAGAAATCTGTATGAGCA 676
Qy 671 ATTCACACAGACTCTGATGTAAGGTATGAGGTCTCCAAAATGACGCCCCCTG 730
Db 677 CAATGAAATGAAAGTACAGCTTTATCTACAGACAAAGCTCCAAAGCATTGTTCCCA 736
Qy 731 TGATCATTTCACTTATGATCATGTGCTATGAGAAAGAACAGAGAGAGACTACTCA 790
Db 737 TGGAGAAATCAGCCAAAGTTTATGATGTC-----AGCTGGGTAAAGCTCTGAA 787
Qy 791 TTCCCTGATCGGTCTATTTAGTTTCTGATGATTTCTGCAATGAGGTTTGTGACCA 850
Db 788 TCCCTGCAAGACATTTCTGCGATTCAGTGAAGAGTGGCCCAATGATCTACTGATGA 847
Qy 851 TTGATGAGAAAAACCTGATGACATATGATGATGATGATGATGATGATGATGATG 910
Db 848 AAGGAGAAAGTTTATGAAAGAACTGAGGTCACATTTAGAAAGGTAAATGAGGCTTC 907
Qy 911 ATAGTAAAGACAGAAAGATGAAACAAAGACTCAGATTTTGTAGCATCAAGAACTTCT 970
Db 908 TCAAGAGACATCTTGAAGAAAGAAAGATGATGATGATGATGATGATGATGATGATG 967
Qy 971 AGATCTGACGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030
Db 968 AAGCTGACCTGCGCAATATATCTGCAATGTTGAAACCGAAATGAGCG-----AAAC 1021
Qy 1031 CAGCCAGATGAGAGAAAGTGGCAAGTCCAAATGATGATGATGATGATGATGATGATG 1090
Db 1022 ATGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1081
Qy 1091 TTGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1150
Db 1082 TGGAGCAGATCTTCT 1141
Qy 1151 AGATGCTCTATTTTACCGGGCTCATTTTGAACAGATGAAACATTTTGAATGAAAG 1210
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Qy 1211 AGTATGATTTATGATCT 1243
Db 1202 AATATGATGCT 1261
Qy 1244 CGAAGAGAGAAATTTGATATGACCTCCGCTGAGATTTTGAAGATGATTTGGAT 1303
Db 1262 CTGAGAGAGAGAGATTTGCTCTGAGATGATGATGATGATGATGATGATGATGATG 1321
Qy 1304 ACAAGCTGTGATCTTTGACCGAGCACTGCTGCGGAGAAATACAGTGAAGCAGTTT 1363
Db 1322 ATAACT 1381
Qy 1364 TTGATTTATCTCAAGAGAGAGAGATGATTTGTTCTGAGCCCTCTCTCTCTCTCT 1423
Db 1382 CAAGATATGTTGACCAAGAGAGAGATGATTTATGTTCTCTCTCTCTCTCTCTCTCT 1441
Qy 1424 AAAAGAGATGAGATGCTGAGTTTAA 1452
Db 1442 GACGGGAGATGATTTTCTGAACTGAA 1470

RESULT 7
US-09-864-761-21077
; Sequence 21077, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21077
; LENGTH: 169
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008249.14
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6
; OTHER INFORMATION: EST HUMAN HIT: AV657306.1, EVALUATE 4.00e-88
; OTHER INFORMATION: NT HIT: AF167340.1, EVALUATE 1.00e-90
; OTHER INFORMATION: SWISSPROT HIT: Q03469, EVALUATE 2.90e+00
US-09-864-761-21077

Query Match 7.2%; Score 149; DB 10; Length 169;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 903 TATTAATGATGATGAGACAGAAATGAAACAAAGCTCAGATTTTGGACATCAAGAAAGT 962
Db 1 TATAAGTATGATGAGACAGAAATGAAACAAAGCTCAGATTTTGGACATCAAGAAAGT 60

Qy	1023	TGGCAAAAGCAGCCAAAGGTGAAAGCAAAAG	1051
Qy	963	TACCTCTGAGGATCTCAAGCCAGACTATGTCTCTCAGTGTAGAAAGTGC	1022
Db	61	TACCTCTGAGGATCTCAAGCCAGACTATGTCTCTCAGTGTAGAAAGTGC	120
Qy	121	TGGCAAAAGCAGCCAAAGGTGAAAGCAAAAG	149
Db			

Thu May 1 09:36:46 2003

us-10-061-727-1.rnpb

Page 8

QY 1114 GNGATTCGATGTTGTTGACATGTTTACGCTGAGATGSGTCCATTTTACGGGGCT 1173
DB 1030 GATGTTGTTGTTGACATGTTTACGCTGAGATGSGTCCATTTTACGGGGCT 1089
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DB 1090 CATTTGGAAGATGAAACATTTTATGAGAAAGATGATTTTATGATCTTAT 1149
QY 1234 GCAAG-----GAAATGCGAGAGAGAGATTTGATTA 1266
DB 1150 ACCAAGTGAATCTGACAGTGAATCAAGACTGGGAGAGAGAGATTTGATTA 1209
QY 1267 CTGACCTCCGTTGAGATTTTGAAGATTTGATCAAGCTGTCATCTTTGACCA 1326
DB 1210 GAAATCTTACCTGATGATGCTTGAAGAGATTTGATGATTTTATGATCAAG 1269
QY 1327 GACAGCTGCTGCGGAGAAATACAGTGAAGAGATTTTGAATTTCAATTCAGAGACAG 1386
DB 1270 GATTTATCTCCAGCTGGAATCATGATTTGAAGATGTCGCAAGATGTCATCAAGCAG 1329
QY 1387 AGATGATGTTGTTGTTGAGCCCTGATCTATGTCAGAGAAAGATGATGCTGAG 1446
DB 1330 CGGCTGATGATGTTGTCAGACCCCAATTAAGTATGAGAGGGGCTGAGCATCTTTGAG 1389
QY 1447 TTTTAA 1452
DB 1390 CTGAGAA 1395

RESULT 9
US-10-011-548-1
Sequence 1, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Tilmans, Jacqueline C.
Debets, Johannes Eduard Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-OCT-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066

FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1737
FEATURE:
NAME/KEY: misc_feature
LOCATION: 342..343
OTHER INFORMATION: /note= "splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 453..454
OTHER INFORMATION: /note= "splice junction"
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LOCATION: 756..757
OTHER INFORMATION: /note= "splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 885..886
OTHER INFORMATION: /note= "splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1033..1034
OTHER INFORMATION: /note= "splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1177..1178
OTHER INFORMATION: /note= "splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1350..1351
OTHER INFORMATION: /note= "splice junction"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-548-1
Query Match 6.8%; Score 139.4; DB 9; Length 1737;
Best Local Similarity 47.8%; Pred. No. 2e-31;
Matches 678; Conservative 0; Mismatches 681; Indels 60; Gaps 7;
QY 64 GAACGTGGAGTACTGGGAGATGACACATGAGGAGAAATCCAGTGTGTAAGATAG 123
DB 70 GATGCTGATGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 126
QY 124 CAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 183
DB 127 CAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 186
QY 184 CATTCAGTGGCTTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 243
DB 187 CAGAGCACTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 244 CCAATTAATCTCCGCTCCCGGAGAAACGATTAAGAGAGAGATGATGATGATG 303
DB 241 CCATCATCT 294
QY 304 CGGCGCACT 363
DB 295 CACTAGCTGAGGACAGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 354

QY 364 TGCAGAAAGTTCATTTCCCTTGAAGTTGTTCAAAAGACAGCTGTTCAATTCCTCC 423
 DB 355 TGCATGAGAGTTCATGTCCTTGAAGTTGTTCAAAAGACAGCTGTTCAATTCCTCC 414
 QY 424 ATGAACTCCAGTGCATTAATCTGTAATGAAATGAGCAATTCAGAGTCTGTTCA 483
 DB 415 AACAGAGTCCGCTATTTAGAAAATCTGAAGTCACTAAAGAAAGAGATCTCTCTCA 474
 QY 484 AATGTATGATGATTTTCTTCCAGTCAAAAGCACTATCACTGTAATGAGCTGT 543
 DB 475 GACATGATGATCTTTAAAGTTCAGAGCTGATGTTGTGTGTAATGAGATGC 534
 QY 544 TATTAATAAGATTTTATATATATATATATATATATATATATATATATATATAT 603
 DB 535 AAGCCAAAATGTGAGAAAGCAATATATATATATATATATATATATATATATATAT 594
 QY 604 GCCTTATTTCAATATATGAAATTAACATGTTGTTTATCATATTCAGAAAATGACGT 663
 DB 595 GTTCAAGAAAGATGAGGAAATTAACATGTTGTTTATATATATATATATATATATAT 654
 QY 664 AGGTTTATCTACCAAGCACTGATGTAAGTATGAGTATGAGTCTTCCAAAATGACGT 723
 DB 655 AAGCAAGCACTGATTTGAAAGTTACAGCTTATCTACAGACAAAGCTTCCAAAGCATTG 714
 QY 724 CCCCCTGATCCATTCACCTATATATATATATATATATATATATATATATATATAT 783
 DB 715 TTCCCATGAGAAATCAGCAAGTGTATATATATATATATATATATATATATATATAT 765
 QY 784 CTATCTATTTCCCTGTAAGTCTATATTTAGTTTCTGATGATTTCTGCAATGAGTTTG 843
 DB 766 CTGAACATCCCTCGAAAGATTTCTGATGAGAGAGTCTGAGGCAATGATCTAC 825
 QY 844 TGGACATTTGATGAGAAAAAAGCTGATGATGATGATGATGATGATGATGATGATG 903
 DB 826 TGGATGAAAGAGAAAAAGTTATATATATATATATATATATATATATATATATATAT 885
 QY 904 ATATAGTAT 963
 DB 886 AGGCTTCTCAAGAGATCTTGAAGAAAAAGATGATGATGATGATGATGATGATGATG 945
 QY 964 ACCTCTGAGATCTCAAGGAGCTATATGTTCTGATGATGATGATGATGATGATGATG 1023
 DB 946 GTTGTGAAAGTGAAGCTGAGGAAATTAATATCTGCTGCTGCTGCTGCTGCTGCTG 999
 QY 1024 GCCAAGCAAGCAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1083
 DB 1000 CGAAGCAAGCAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1059
 QY 1084 TGTGTTTGAAGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1143
 DB 1060 GGGGCTGAGGAGCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1119
 QY 1144 TGGCTAGAGATGCTTATTTTACCGGCTCATTTTGAACAGATGAACATTTTGAAT 1203
 DB 1120 AACATTTGAATGATGCT 1179
 QY 1204 GGAAGAGATGAT 1239
 DB 1180 AACAGAGATGAT 1239
 QY 1240 AATGCGAAGAGAGATTTTATATATATATATATATATATATATATATATATATAT 1296
 DB 1240 GACATCTCTGAG 1299
 QY 1297 TTTGATACAGAGCTGATCTTTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353
 DB 1300 TATGAT 1359
 QY 1354 GAAAGAGTTTAT 1413
 DB 1360 GAAATCTCAAGAT 1419

QY 1414 TATGTACAGAAAGATCAGATGCTGAGTTTAA 1452
 DB 1420 TATATCTCAGACGGAGATGAGTATTTTGAATCGAA 1458

RESULT 10
 US-09-880-107-3616/c
 ; Sequence 3616, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Iwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-WO
 ; CURRENT APPLICATION NUMBER: US/09/880,107
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3616
 ; LENGTH: 443
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 W85847
 ; NAME/KEY: unsure
 ; LOCATION: (1)-(443)
 ; OTHER INFORMATION: n = a or c or g or t
 ; US-09-880-107-3616

Query Match 5.5%; Score 113.6; DB 10; Length 443;
 Best Local Similarity 89.4%; Pred. No. 5.8e-24;
 Matches 144; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 893 TTAAGGAAAGTATAGTCTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 951
 DB 442 TTAAGGAAAGTATAGTCTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
 QY 952 ATCAAGAAAGTATACCTGAGAGATCT-CAAGCGAGTATGCTGATGATGAGAGTGC 1010
 DB 382 ATCAAGAAAGTATACCTGAGAGATCTCAAGCGAGTATGCTGATGATGAGAGTCC 323

QY 1011 CAAGCGAGAGTTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1051
 DB 322 AAAGCGAAGTTGCCAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 282

RESULT 11
 US-09-864-761-4326
 ; Sequence 4326, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wenheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
 ; FILE REFERENCE: Aecmica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 4326
LENGTH: 400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008249.14
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6
US-09-864-761-4326

Query Match 4.6%; Score 95; DB 10; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 901 AGTAACTCTAGTAAAGAAAGATGAAGAACTCAGATTGAGCATCAAGAA 960
DB 306 AGTAACTCTAGTAAAGAAAGATGAAGAACTCAGATTGAGCATCAAGAA 365
QY 961 GTTAACTCTGAGATCTCAAGCGCAGCTATGCTG 995
DB 366 GTTAACTCTGAGATCTCAAGCGCAGCTATGCTG 400

Result 12
US-09-981-421-3
Sequence 3, Application US/09981421
Patent No. US20020098185A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Mohler, Kendall M.
TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
FILE REFERENCE: 3086-A
CURRENT APPLICATION NUMBER: US/09/981,421

CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1626
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1626)
OTHER INFORMATION:
US-09-981-421-3

Query Match 4.3%; Score 89.6; DB 10; Length 1626;
Best Local Similarity 46.3%; Pred. No. 2.9e-16;
Matches 391; Conservative 0; Mismatches 429; Indels 24; Gaps 2;

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QY 724 CCCCCTGTGATTCATTCACCTAATGATCATGTGCTTATGAAAGAACCGAGAGAG 783
DB 643 CCGGTTCTTCTGAGCAAAAGCTTAACCATGTGCGAGTAATTAAGAAAAAGTAAG 702
QY 784 CTACTATTCCTGTAAGGCTATTTAGTTTCTGATGATCTGCAATGAGTTTGG 843
DB 703 CTCACTGCTCTGCTTGTGTAATGAAGAGATTAATTAATGATTTGGGAGAA 762
QY 844 TGACCAATGAGAAAAAACCCTGATGACATCATATTGATGTCACATTAAGAAAT 903
DB 763 AATGATCGGATCTTAATTAATGATGAAGAAAGAAATGATTAATGATCCAGAAAG 822
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DB 943 AGAAAGCAGACATGCTGATATCCAGGCCAGCTCTTCAAGAGAGATGATATAGCT 1002
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DB 1174 GAGACACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1233
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Db 1294 CTGATGAGAAAGCCGAGACTAATCATTTCTTAAGTAAAGTATATGCTAATAG 1353
 Qy 1429 AGCA 1432
 Db 1354 GTCA 1357

RESULT 13
 US-10-157-447-1

; Sequence 1, Application US/10157447
 ; Patent No. US20020143155A1

GENERAL INFORMATION:

APPLICANT: Parneet, Patricia et al.

TITLE OF INVENTION: Receptor Designated 2F1

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/157,447

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/578,178

FILING DATE: <Unknown>

APPLICATION NUMBER: 09/110,618

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1626 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: hu2F1

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1626

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 58..1623

FEATURE:

NAME/KEY: sig_peptide

LOCATION: 1..57

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-157-447-1

Query Match 4.3%; Score 89.6; DB 12; Length 1626;

Best Local Similarity 46.3%; Pred. No. 2.9e-16;

Matches 391; Conservative 0; Mismatches 429; Indels 24; Gaps 2;

Qy 604 GCCTTAATTCATAATGAAATTCACATGTGTGTTCATATCCAGAAATGACGT 663

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Db 523 GCCGAGTTTGAAGATCAGGGATATTACTCCGTCGTCATTTCTTCATATATGAAAA 582

Qy 664 AGCTTCATCTGACGACGAGCTGCACTGTAAGAGTAGAGCTCCCAAAAAATGACGTG 723

Db 583 CTATTTAATATCAACAAACCTTCATATACAAATATGGAAGATCGCATATATATGTT 642

Qy 724 CCCCCGTGATCCATTCACCTAATATGATCATGTGCTATAGAAAACAGAGAGAG 783

Db 643 CCGGTTCTCTTGAGACCAAGCTTAACATGTTGACGTGGAATTTGAAAAACGTAAG 702

Qy 784 CTATCATTCCTGTAAGGTCTAATTTAGTTTCTGATGATTTCTGCAATGAGTTGG 843

Db 703 CTCACCTGCTCTGCTTTGCTGATGAAAGATGTAATTTATTTGATGTTGGGAAAGA 762

Qy 844 TGGACCATTTGAGAAAAAACCTGATGACATCATTTAGTCACTTAACGAAGT 903

Db 763 AATGATCGAATCTTAATATACATAAGAAAGAAATGAAATTAATGATCTCAGAGGC 822

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Db 823 AATGCAATGCTTCAAAAGTATTTGAAATGAAATTTGTAAGCAATCTAATATGTT 882

Qy 964 ACCTTGAGATCTCAAGCGCATATGCTGTCATGCTAGTAGAGCCAAAGCGAAGTT 1023

Db 883 TTAATTAATTCATCTGTCGACAGCAGGAGGACAGACACCAAAAGCTTCATCTTG 942

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Qy 1144 TGGCTAGAGATGCTCTATTTTACCGGCTCATTTTGAAGATGAAACCATTTAGAT 1203

Db 1063 T-----TGGTCTATTTATGACATTTAAGCAAGAAAGATGAAACATTAACAGAT 1113

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Qy 1249 GAAGAAGATTTGTATTTACTGACCTCGTGAGTTTGAAGATGAAATTTGATATCAAG 1308

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Qy 1309 CTGTGATCTTTGACGAGACAGTCTGCTGAGGAAATACAGTGAAGCACTTTTAT 1368

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Db 1294 CTGATGAGAAAGCCGAGACTAATCATTTGCTTAAGTAAAGTATATGCTAATGAG 1353

Qy 1429 AGCA 1432

Db 1354 GTCA 1357

RESULT 14

US-09-764-853-235

; Sequence 235, Application US/09764853

; Patent No. US20020090672A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: P1206

CURRENT APPLICATION NUMBER: US/09/764,853

Prior application data removed - consult PAM or file wrapper

NUMBER OF SEQ ID NOS: 939

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 235

Thu May 1 09:36:46 2003

us-10-061-727-1.rnpb

Page 12

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; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-235

Query Match
Best Local Similarity 52.8%; Score 88.6; DB 10; Length 1977;
Matches 236; Conservative 0; Mismatches 184; Indels 27; Gaps 1;

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DB 389 GCCAGGGTCTCTCTTCAATAAACGAGAGCTAATGTACACAGTGAAGCTTGGAGGCCCTT 448
QY 1093 GGAGCCACAGCTCTGCTAGTGGTATTCATTTGTTTACATGTTTACAGTGGTAAAG 1152
DB 449 GGTGCTATCTCTGCTGCTTGTATGTGTGTCACCATCTTCAAGTGTACAAAGATGAA 508
QY 1153 ATGCTCTATTTTACCGGCTCATTTTGGAAACAGATGAACCATTTTACATGGAAGAG 1212
DB 509 ATCATGCTCTTCAAGAGATCATTTTGGAGCTGAAGAGCTGATGAGACATTAAGAT 568
QY 1213 TATGATATTATGATCTCT-----ATGCAAGGAATGCG 1245
DB 569 TATGATGCAATCTTATCATACACCAAGTGAATCTGACCAAGTGAATCAAGAGCTGG 628
QY 1246 GAAGAAAGAAATTTGATTAATCTGACCTCCGCGAGTTTGGAGATGAATTTGATAC 1305
DB 629 GAAGAAAGAAAGTTTGGCTTGAATCTGATATGCTTGAAGAAAGCTATTAAGATAT 688
QY 1306 AAGCTGTGATCTTTTACCGAGACAGCTGCTGGGGAAATACAGTGAAGAGATTTT 1365
DB 689 AATGTTTATACCAAGATGAGATTAATCCACAGTGAACATACATGAGATGAGCA 748
QY 1366 GATTTCAATCAGAAAGAGAGATGTTGTTCTGAGCCCTGATCTATGTGACAGAA 1425
DB 749 AGATGTGTAGATCAAGCAAGCGCTGATATGTGATGACCCCAATTAAGTATGAG 808
QY 1426 AAGAGATCAGCAGCTGCTGGAGTTTAA 1452
DB 809 AGGGCTGAGCAATCTTGAAGTGA 835

RESULT 15
US-10-011-548-19
; Sequence 19, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,548
; FILING DATE: 22-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/173,151
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1991 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1458
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-011-548-19

Query Match
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Matches 236; Conservative 0; Mismatches 184; Indels 27; Gaps 1;

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QY 1153 ATGCTCTATTTTACCGGCTCATTTTGGAAACAGATGAACCATTTTACATGGAAGAG 1212
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QY 1213 TATGATATTATGATCTCT-----ATGCAAGGAATGCG 1245
DB 583 TATGATGCAATCTTATCATACACCAAGTGAATCTGACCAAGTGAATCAAGAGCTGG 642
QY 1246 GAAGAAAGAAATTTGATTAATCTGACCTCCGCGAGTTTGGAGATGAATTTGATAC 1305
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QY 1306 AAGCTGTGATCTTTTACCGAGACAGCTGCTGGGGAAATACAGTGAAGAGATTTT 1365
DB 703 AATGTTTATACCAAGATGAGATTAATCCCAATGGAACATACATTAAGATGAGCA 762
QY 1366 GATTTCAATCAGAAAGAGAGATGTTGTTCTGAGCCCTGATCTATGTGACAGAA 1425
DB 763 AGATGTGTAGATCAAGCAAGCGCTGATATGTGATGACCCCAATTAAGTATGAG 822
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DB 823 AGGGCTGAGCAATCTTGAAGTGA 849

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 07:18:20 ; Search time 1999 Seconds
(without alignments)
16722.103 Million cell updates/sec

Title: US-10-061-727-1

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Sequence: 1 atgacactctgtgtgtgtc.....acgactttatccctataa 2064

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Indexed: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estm:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
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- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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3	701.6	34.0	873	13	B1662501 B1662501
4	632.2	30.6	814	14	B0006059 UI-H-E11-
5	601.2	29.1	880	13	B1330085 B1330085
6	513.8	24.9	923	9	AL544533 AL544533

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8	501	24.3	789	10	AV659167	AV659167
9	500.4	24.2	756	6	A1303998	A1303998
10	499.6	24.2	723	10	AW211290	AW211290
11	490.8	23.7	910	12	BB892231	BB892231
12	489	23.8	489	14	BM760155	BM760155
13	486.4	23.6	580	13	B1346913	B1346913
14	453	21.9	888	13	B1331848	B1331848
15	413	20.0	652	10	BB625831	BB625831
16	406.8	19.7	533	9	AA239486	AA239486
17	405.8	19.7	598	9	AA237107	AA237107
18	399.2	19.3	643	9	AA107505	AA107505
19	396.8	19.2	676	10	BB626271	BB626271
20	396.8	19.2	643	10	BB653335	BB653335
21	390.8	18.9	616	10	AV661936	AV661936
22	383.4	18.6	646	10	BB612046	BB612046
23	382.2	18.5	396	14	T08277	T08277
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ACCESSION	BC016141				
VERSION	BC016141.1	GI:16359373			
KEYWORDS	HTC.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DCPD/BTP CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,				

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 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."
 BASE COUNT 249 a 215 c 193 g 223 t
 ORIGIN

Query Match 29.1%; Score 601.2; DB 13; Length 880;
 Best Local Similarity 83.9%; Pred. No. 3.2e-167;
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Qy 974 ATCTCAGCGCA 985
 Db 841 ATCTCAGCGCA 852

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 VERSION AL544533.1 GI:12877013
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Peng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : Elliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 226 a 99 c 323 g 218 t 57 others
 ORIGIN

Query Match 24.9%; Score 513.8; DB 9; Length 923;
 Best Local Similarity 86.7%; Pred. No. 3.7e-141;
 Matches 547; Conservative 32; Mismatches 49; Indels 3; Gaps 2;

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294 TTGAAGAGTTGTTGAATTAAGTAAGGASAGAGGATTTAGGAGGTTAG 353
208 TGTATTGACATGACGAGACCGGACCTTGAAGACCAATTAACCTCCCGAG 267
354 TGTATTGASATGAGGRRGGGGGGGGGTTGAGAGGGAATTAAGTTGGGG 413
268 AACCGATTAGTAAGAGAAAGATGTGCTGTCCG--GCCACTCTCCCATG 325
414 AAGGSGATTAGTGRGGRGARGATGTGGGTTGGGGGCGCASTSSATGACA 473
326 CTGGCAACTATACCTGCAATTAAGGAACATACATATTTGAGCAAGAATG 385
474 CTGGGAACATACCTGCAATTAAGGAACATACATATTTGAGGATTTSSST 533
386 TGAAGTTGTTCAAAAAGACAGCTGTTCAATTTCCCAATGAACTCCAGT 445
534 TGAAGTTGTTCAAAAAGACAGCTGTTCAATTTCCCAATGAACTCCAGT 593
446 TGTATTAGAAATATGACATTCAGAGATCACTTGTCCAAATGATGATGAT 505
594 TGTATTAGAAATATGACATTCAGAGATCACTTGTCCAAATGATGATGAT 653

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QY 618 TAATGAAATTAACATGCTGTGTTACATATCCAGAAATAGACGTATTCATCTCAC 677
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 DB 662 CANGACTGTGACTGTAAATGTGTGAGCTACCAAA 696
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 LOCUS u079807.y1 NCI CGAP Mam3 Mus musculus cDNA clone IMAGE:2648725.5,
 DEFINITION similar to gb:X85999.M.musculus mRNA for interleukin 1 receptor
 ACCESSION AM211290.1 GI:6517238
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 723)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at:
 www.bio.liml.gov/db/ftp/image/image.html
 MGI:1029177
 Seq primer: -40RP from Gibco
 High quality sequence stop: 427.
 Location/Qualifiers
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 /strain="129, C57BL/6J, FVB/N"
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 /tissue_type="tumor, gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies, Inc. Investigators
 providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."
 BASE COUNT 206 a 148 c 182 g 186 t 1 others
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 Best Local Similarity 82.4%; Pred. No. 5.3e-137;
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 QY 744 TAATGATCATGTGCTTATAGAAAGACGAGAGAGACTATCTCATTCCTGTACGGT 803

DB 121 AATGACCGTGTGCTATAGAAAGAACAGAGAGAACTGTATTCCTGCAAGT 180
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 DB 181 CTATTTCACTTTCAATATGACTCCCAATAGAGGTGTGTGACCATGATGAAAAA 240
 QY 864 ACCGTATGACATCACTATTTGATGTCACCAATTAAGCAATTAAGTATGAGACAGA 923
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 QY 924 AGATGAACAAGAACTCAGATTTTGTAGCATCAAGAAAGTTACTTGTAGATTCGA 983
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 QY 1224 TGTATCTTATGCAAGATGCGGAGAGAGAGATTTGATTTACTGAC-CCTCCGTGAG 1282
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 QY 1343 GAA 1345
 DB 720 GAA 722
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 ACCESSION BE892231
 VERSION BE892231.1 GI:10352355
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 910)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DRP
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at:
 http://image.liml.gov
 Plate: LIM9751 row: a column: 17
 High quality sequence stop: 710.
 Location/Qualifiers
 1..910
 /organism="Homo sapiens"

Thu May 1 09:36:47 2003

us-10-061-727-1.rst

Page 10

Oy	707	CTCCAAAAATCAGTGCCTCCGTGATCATTCAGCTAATGATCATGTGCTATGGA	766
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Db	361	CTCGAATGAGGTTTGTGTGACCATTTGATGAAAAAACTGATGACATCATATTGATG	420
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DEFINITION	376288 MARC 2P1G Sus scrofa CDNA 5' , mRNA sequence.
ACCENSION	B1346913
VERSION	B1346913..1 GI:15040211
KEYWORDS	
SOURCE	EST.
	Pig.

ORGANISM	Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.	
1 (bases 1 to 580)	
REFERENCE	
AUTHORS	Fahnenkrug, S. C., Freking, B. A., Rohrer, G. A., Smith, T. P. L., Casas, E.,

TITLE
JOURNAL
COMMENT

Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keeler, J.W.
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
Unpublished (2000)
Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: smithe@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mscore 18
and -mismatch 12 options.

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PCR PRIMERS
FORWARD: AGGAACAGCTATGATGCCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 130 row: L column: 3
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          Location/Qualifiers
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/clone_id="MARC 2P1G"
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/lab_host="DH10B"
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library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      159 a      110 c      158 g      153 t
ORIGIN

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Query Match	23.6%	Score 486.4	DB 13	Length 580
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Db	2	AGATGAGACAAGGACCTACGACTTTTGAGATCAAG- AAGTAACTGCTGAGATCTCAAGCG	60
Oy	984	CAGCTATCTCTGTATGCTAGAGATGCCAAGGCGAAGTTGCCAAGACGCAAGGTGAA	1043
Db	61	CAACTATCTCTGTATGCTAGAGATGCCAAGGCGAAGTTGACAGACCGGCGCAAGGTGAA	120
Oy	1044	GCAGAAATGCGACGCTCCAAATATACAGGTGGAACCTGGCTTGCGTTTGGAGGCACAGT	1103
Db	121	ACAGAA-----ACTCCCAATATACAGGTGGAACCTGGCAATGCGTTTGGAGGCACAGT	174
Oy	1104	CTGTCTAGTGGNGATCTTCATTTGTTGTTTACATGTTTACTCGGCTAGAGATGTCCTAAT	1163
Db	175	CTGTGATGATGATATCTCATTTGTTGTTTACATGTTTACTCGGCTGAGATGCTCTCTT	234
Oy	1164	TTACCGGCGCTCATTTTGGAAACAGATGAACCATTTTAGATGAAAGAGTATGATATTTA	1223
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Oy	1224	TGTATCTTATGCAAGAAATGCGGAAGAAAGAAATTTGTATTACTGACCTTCCTGGAGT	1283
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Oy	1284	TTTGGAGAAATGAATTTGGAATACAGCTGTGTGATCTTTGACCGGACAGCTCTGGCGGGGG	1343
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Oy	1344	AAATACAGTGAAGCAGTTTGTGATTTTCATTCAAGAGAAGCAGAAAGATGTTGTGTCT	1403
Db	415	AAATACGCTGGAACAGTTTGTGATTTTCATTCAAGAGACCGGAGAGATGTTGTGTCT	474
Oy	1404	GAGCCCTGACTATGTGAAGAGAAAGAGATCAGATGCTGAGGTTTAAACTGGGTTGAT	1463
Db	475	GAGCCCAAGACTATGTGAAGAGAAAGAGATCAGATGCTGAGGTTTAAAGCTGGGTTGAT	534
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RESULT 14
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DEFINITION      602982528F1 NCI CGAP_i19 Mus musculus cDNA clone IMAGE:5135287 5',
ACCESSION      BI331848
VERSION        BI331848
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

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Query Match 20.0%; Score 413; DB 10; Length 652;
 Best Local Similarity 87.3%; Pred. No. 3.2e-111;
 Matches 452; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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QY 1 ATGACACTTCGTGAGTGTGATGATGATCTCACTTTATGGAATCCCTGCAAAAGTATGCC 60
DB 133 ATGGAGCTTCGTGAGTGTGATGATGATCTCACTTTATGGAATCCCTGCAAAAGTATGCC 60
QY 61 TCAGAAAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 193 TCAGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 252
QY 121 GAGCGAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 253 GAGCGAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
QY 181 GCCCATTCAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 313 GCCCATTCAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
QY 241 GAGCGATTCAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 373 GAGCGATTCAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
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DB 433 TTCGGGCGGCACTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 492
QY 361 TATTCAGAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 493 TATTCAGAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
QY 421 CCATGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 553 CCATGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 612
QY 481 CCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 518
DB 613 CCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
    
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Search completed: April 30, 2003, 09:40:11
 Job time : 2012 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 23, 2003, 08:44:05 ; Search time 40 Seconds

(Without alignments)
2288.579 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLKMCVSLYFYGLQSDA.....SALALHFTDLNNNDPYIL 687

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 908470

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2586	70.5	570	22	AAU09966 Human interleukin-
2	2586	70.5	570	23	AAE16590 Human interleukin-
3	2586	70.3	550	22	AAU09978 Human IL-1R ACP pr
4	2580	70.3	570	17	AAW01911 Human interleukin-
5	2559	69.7	540	22	AAU09979 Human IL-1R ACP pr
6	2527	68.9	530	22	AAU09980 Human IL-1R ACP pr
7	2525	68.8	559	22	AAU09973 Human IL-1R ACP pr
8	2502.5	68.2	512	22	AAU09987 Human IL-1R ACP pr
9	2502.5	68.2	520	22	AAU09981 Human IL-1R ACP pr
10	2327.5	63.4	570	17	AAW01913 Mouse interleukin-

11	2327.5	63.4	570	22	AAU09967	Mouse interleukin-
12	2327.5	63.4	570	23	AAE16576	Mouse interleukin-
13	2243	61.1	508	22	AAU09974	Human IL-1R ACP pr
14	2212	60.3	501	22	AAU09982	Human IL-1R ACP pr
15	1934	52.7	359	17	AAW01912	Soluble interleukin
16	1930	52.6	910	21	AAI92206	Fusion polypeptide
17	1923	52.4	450	22	AAU09975	Human IL-1R ACP pr
18	1889	51.5	356	19	AAW53897	Human interleukin-
19	1648	44.9	400	22	AAU09983	Human IL-1R ACP pr
20	1429	38.9	360	22	AAU09976	Human IL-1R ACP pr
21	1053	28.7	290	22	AAU09984	Human IL-1R ACP pr
22	888	24.2	260	22	AAU09977	Human IL-1R ACP pr
23	825	22.5	686	20	AAI14128	Human IL-1R ACP pr
24	825	22.5	686	23	AAE16567	Human interleukin-
25	817.5	22.3	658	20	AAI22143	Human TIGIR prote
26	800	21.8	579	20	AAI14130	Human IL-1R ACP pr
27	800	21.8	579	23	AAE16566	Human interleukin-
28	793	21.6	240	22	AAU09985	Human IL-1R ACP pr
29	767.5	20.9	696	21	AAI95288	Human Xrec2. Homo
30	767.5	20.9	696	22	AAW78808	Human protein SEQ
31	767.5	20.9	710	22	AAE11785	Human oligophrenin
32	767.5	20.9	710	22	AAW79792	Human interleukin-
33	762.5	20.8	668	23	AAE16589	Human interleukin-
34	558.5	15.2	152	22	AAU09988	Human IL-1R ACP pr
35	543	14.8	190	22	AAU09986	Human IL-1R ACP pr
36	528.5	14.4	540	19	AAW71145	Human interleukin-
37	528.5	14.4	540	20	AAI93976	Interleukin-18 rec
38	528	14.4	541	18	AAW11907	Human receptor pro
39	528	14.4	541	20	AAI06613	Human interleukin-
40	528	14.4	541	23	AAE14731	Human IL-18 recept
41	528	14.4	541	23	AAE16583	Human interleukin-
42	520	14.2	521	20	AAI93980	Interleukin-18 rec
43	496	13.5	555	23	AAE16587	Chicken interleukin
44	484.5	13.2	576	15	AAE59091	Mouse interleukin-
45	484.5	13.2	576	15	AAE60869	Murine IL-1 recept

ALIGNMENTS

RESULT 1					
AAU09966	ID	AAU09966 standard; Protein; 570 AA.			
XX	XX	AAU09966;			
XX	AC	21-MAY-2002 (first entry)			
XX	DT	Human interleukin-1 Receptor accessory protein (IL-1R ACP) protein.			
XX	XX	IL-1; IL-1RI; Immunogen; inflammatory response.			
KW	XX	IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;			
XX	OS	Homo sapiens.			
XX	Key	Location/Qualifiers			
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FT	Region	235..281			
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FT	Region	238..252			
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FT	Region	322..338			

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FT      28-AUG-2001.
FT      16-DEC-1997; 97US-0991944.
FT      16-DEC-1997; 97US-0991944.
FT      16-DEC-1997; 97US-0991944.
FT      (TUL- ) TULARIK INC.
FT      Cao Z;
FT      MPI: 2001-595441/67.
FT      N-PSDB; AAS15608.
FT      Isolated polypeptide designated interleukin receptor accessory
FT      polypeptide is useful for regulating cell function
FT      Claim 1; Fig 1; 21pp; English.
XX      This sequence represents the human interleukin-1 receptor accessory
XX      protein (IL-1Racp) of the invention. The interleukin receptor
XX      accessory protein (IL-1Racp) and its modulators (agonists/antagonists)
XX      are useful for regulating cell function. Transient expression of either
XX      IL-1RI or IL-1Racp alone does not result in ligand-independent induction
XX      of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
XX      coexpression of both proteins resulted in a 20-fold increase in
XX      activation of NF-kappaB activity to a level comparable to that induced
XX      by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as
XX      a result of protein overexpression can elicit a signaling pathway
XX      leading to NF-kappaB activation. Modulating signal transduction
XX      involving NF-kappaB in a cell may be achieved by modulating the activity
XX      of IL-1Racp using binding agents such as agonists and antagonists.
XX      Hybridisation probes to the cDNA sequence can be used to identify wild-
XX      type and mutant IL-1Racp alleles in clinical and laboratory
XX      samples. Mutant alleles are used to generate allele-specific
XX      oligonucleotide (ASO) probes for high-throughput clinical diagnoses
XX      of diseases or disorders with an inflammatory response. In
XX      therapy, therapeutic IL-1Racp nucleic acids are used to modulate
XX      cellular expression or intracellular concentration or availability of
XX      active IL-1Racp. This invention also comprises a method of screening for
XX      an agent that modulates the interaction of an interleukin receptor
XX      accessory polypeptide (IL-1Racp) to a binding target.
XX      Sequence 570 AA;
XX      Query Match 70.5%; Score 2586; DB 22; Length 570;
XX      Best Local Similarity 85.3%; Pred No. 1,4e-212;
XX      Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

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DB      121 YCSKVAFLPVLVQKSCFNSPKMLPVHKLIEYGIQIRICPNVDGFPSSVKTITWNG 180
DB      181 CYKIQNFNNVDEGNMLSTLALISNNGVTCVTVY PEGRTFHLTRLLTVKVSPPKNA 240
DB      181 CYKIQNFNNVDEGNMLSTLALISNNGVTCVTVY PEGRTFHLTRLLTVKVSPPKNA 240
DB      241 VPPVHSPNDHVYKEPEBELLIPCTVYFSLMDSRNWMTTIDCKRDDITIDVTINE 300
DB      241 VPPVHSPNDHVYKEPEBELLIPCTVYFSLMDSRNWMTTIDCKRDDITIDVTINE 300
DB      301 SISHSRTDETRTQILSIKVTSEDLKRSYVCHASAKGEVAKAAVKOKVAPRYTVEL 360
DB      301 SISHSRTDETRTQILSIKVTSEDLKRSYVCHASAKGEVAKAAVKOKVAPRYTVEL 360
DB      361 ACGFGATVLLVYLIVVHYVWLEWLFYRAHGTDETLIDKEKXDIYVSARNAEEEF 420
DB      361 ACGFGATVLLVYLIVVHYVWLEWLFYRAHGTDETLIDKEKXDIYVSARNAEEEF 420
DB      421 VALLTARGVLENERGYKLCIFDRDSLPGCNTVAEVPDIORSRMIVVLSPTYTEKISIM 480
DB      421 VALLTARGVLENERGYKLCIFDRDSLPGCNTVAEVPDIORSRMIVVLSPTYTEKISIM 480
DB      481 LEPKLGVMCONSIAATK---LIVVEYRPLEHPHGLQKES---VSPVSMGKSKHSG 533
DB      481 LEPKLGVMCONSIAATK---LIVVEYRPLEHPHGLQKES---VSPVSMGKSKHSG 533
DB      534 SKFWKALRLALPLRLSLASGSGNESCSSQSDI 565
DB      536 GRFMKQLQVAMPVKKSPRRSSDEQLSYSSL 567
XX      RESULT 2
XX      ID AAE16590 standard; Protein; 570 AA.
XX      AAE16590;
XX      AA016590;
XX      09-APR-2002 (first entry)
XX      Human interleukin-1 receptor DNAX designation 3 (IL-1RD3) protein.
XX      Human; morphogenesis; immune system; interleukin-1 DNAX designation 3;
XX      IL-1RD3 protein; therapy; immunological disorder.
XX      Homo sapiens.
XX      US6326472-B1.
XX      04-DEC-2001.
XX      14-OCT-1998; 98US-0173151.
XX      15-OCT-1997; 97US-062066P.
XX      17-NOV-1997; 97US-065776P.
XX      12-MAR-1998; 98US-078008P.
XX      18-MAR-1998; 98US-078416P.
XX      15-APR-1998; 98US-081883P.
XX      10-AUG-1998; 98US-095987P.
XX      (SCHE ) SCHERING CORP.
XX      Timans JC, Debets JEMA, Sana TR, Bazan JF, Kastelein RA;
XX      MPI; 2002-121110/16.
XX      Antibody fragments which specifically bind to primate interleukin 1
XX      receptor-like molecules are useful to treat conditions associated with
XX      abnormal expression of the receptor or its ligand, particularly
XX      immunological disorders
XX      Disclosure; Column 51-54; 102pp; English.

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CC The present invention relates to compositions and methods for affecting
 CC mammalian physiology such as morphogenesis of immune system function.
 CC The invention particularly relates to nucleic acids, proteins and
 CC antibodies which regulate development and/or the immune system. The
 CC invention also relates to antibody fragments which specifically bind
 CC to antigenic fragments of a primate interleukin (IL)-1 receptor like
 CC molecules such as IL-1 receptor DNAx designation (IL-1RD). The antibody
 CC fragments of the invention are useful to treat conditions exhibiting
 CC abnormal expression of the receptors or their ligands which typically
 CC will be immunological disorders. The present sequence is human IL-1RD3
 CC protein.

CC
 XX
 SQ Sequence 570 AA;

Query Match 70.5%; Score 2586; DB 23; Length 570;
 Best Local Similarity 85.3%; Pred. No. 1.4e-212;

Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

1 MTLMCVSLVYFGILQSDASERCDWGLDTRQIQVFEDPARIKCPLEHFLKENVST 60
 1 MTLMCVSLVYFGILQSDASERCDWGLDTRQIQVFEDPARIKCPLEHFLKENVST 60
 61 AHSAGTLTIWYTRQDRLEBPINFLPENNRSKEKDVLMFRPTLNDGNTTQMLRNTT 120
 61 AHSAGTLTIWYTRQDRLEBPINFLPENNRSKEKDVLMFRPTLNDGNTTQMLRNTT 120
 121 YCSKVAPELEVVOQSCFNSPMKLPVHKLYIEYGIQRTCPNDVGYPSSVAPRTITWNG 180
 121 YCSKVAPELEVVOQSCFNSPMKLPVHKLYIEYGIQRTCPNDVGYPSSVAPRTITWNG 180
 181 CYKIONFNNVIEPEGNNLSFLIALISNNGNYTCVTPYPNGRTFHLTRTLTVKVGSSPKNA 240
 181 CYKIONFNNVIEPEGNNLSFLIALISNNGNYTCVTPYPNGRTFHLTRTLTVKVGSSPKNA 240
 241 VPPVHSPNDHVVYEKEPEEELIIPCTVYFSPILMDSRNEVMTIDGKDDITITVTINE 300
 241 VPPVHSPNDHVVYEKEPEEELIIPCTVYFSPILMDSRNEVMTIDGKDDITITVTINE 300
 301 SISHSTREBETQTOLISIKKTSSEDKRSYVCHABSAKEVAKAAVKKVAPRTYVEL 360
 301 SISHSTREBETQTOLISIKKTSSEDKRSYVCHABSAKEVAKAAVKKVAPRTYVEL 360
 361 ACSPGATVLLVVLIVVYVYVLEWLPFRAHGTDETLIDGKEVYIYSVARNABEEEF 420
 361 ACSPGATVLLVVLIVVYVYVLEWLPFRAHGTDETLIDGKEVYIYSVARNABEEEF 420
 421 VLLTRAGVLENEFGYKLCIFDRDSLPGGNTVAVPDPIQSRSMIVLSPDYVTEKSISM 480
 421 VLLTRAGVLENEFGYKLCIFDRDSLPGGNTVAVPDPIQSRSMIVLSPDYVTEKSISM 480
 481 LEFKLGWMCQNSIATK---LIVVERPLEHPHGLQLES---VSFVSWKGEKSKHSG 533
 481 LEFKLGWMCQNSIATK---LIVVERPLEHPHGLQLES---VSFVSWKGEKSKHSG 533
 534 SKFWKALRLALPLRLSASSGNWSSSSOSDI 565
 534 SKFWKALRLALPLRLSASSGNWSSSSOSDI 565
 536 GRPWKQLQVAMFVKKSPRRSSDDEGLSTYSL 567
 536 GRPWKQLQVAMFVKKSPRRSSDDEGLSTYSL 567

RESULT 3
 ID AAU09978 standard; Protein; 550 AA.
 ID AAU09978 standard; Protein; 550 AA.

AAU09978;
 21-MAY-2002 (first entry)

Human IL-1R ACP protein deletion mutant delta CI.

IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;
 IL-1; IL-1RI; mutant; delta CI; inflammatory response.

OS Homo sapiens.

XX US6280955-B1.
 PN 28-AUG-2001.
 XX 16-DEC-1997; 97US-0991944.
 XX 16-DEC-1997; 97US-0991944.
 XX (TULIA-) TULARK INC.
 XX Cao Z;
 XX WPI; 2001-595441/67.
 DR N-PESDB; AAS15608.

PT Isolated polypeptide designated interleukin receptor accessory
 PT polypeptide is useful for regulating cell function

Disclosure; Page - : 21pp; English.

CC This sequence represents the human interleukin-1 receptor accessory
 CC protein (IL-1Racp) mutant delta CI of the invention. This mutant
 CC was used to define domains of the IL-1Racp protein that have the
 CC ability to activate NF-kappaB expression. The interleukin receptor
 CC accessory protein (IL-1Racp) and its modulators (agonists/antagonists)
 CC are useful for regulating cell function. Transient expression of either
 CC IL-1R or IL-1Racp alone does not result in ligand-independent induction
 CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
 CC coexpression of both proteins resulted in a 20-fold increase in
 CC activation of NF-kappaB activity to a level comparable to that induced
 CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as
 CC a result of protein overexpression can elicit a signaling pathway
 CC leading to NF-kappaB activation. Modulating signal transduction
 CC involving NF-kappaB in a cell may be achieved by modulating the activity
 CC of IL-1Racp using binding agents such as agonists and antagonists.
 CC Hybridisation probes to the cDNA sequence can be used to identify wild-
 CC type and mutant IL-1Racp alleles in clinical and laboratory
 CC samples. Mutant alleles are used to generate allele-specific
 CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
 CC of diseases or disorders with an inflammatory response. In
 CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
 CC cellular expression or intracellular concentration or availability of
 CC active IL-1Racp. This invention also comprises a method of screening for
 CC an agent that modulates the interaction of an interleukin receptor
 CC accessory polypeptide (IL-1Racp) to a binding target.
 CC Note: The present sequence is not included in the
 CC specification but was created from the human IL-1R ACP sequence
 CC appearing as AAU09966 and the information given in table 1 of the
 CC specification.

SQ Sequence 550 AA;

Query Match 70.3%; Score 2580; DB 22; Length 550;
 Best Local Similarity 87.4%; Pred. No. 4.4e-212;

Matches 484; Conservative 33; Mismatches 25; Indels 12; Gaps 4;

1 MTLMCVSLVYFGILQSDASERCDWGLDTRQIQVFEDPARIKCPLEHFLKENVST 60
 1 MTLMCVSLVYFGILQSDASERCDWGLDTRQIQVFEDPARIKCPLEHFLKENVST 60
 61 AHSAGTLTIWYTRQDRLEBPINFLPENNRSKEKDVLMFRPTLNDGNTTQMLRNTT 120
 61 AHSAGTLTIWYTRQDRLEBPINFLPENNRSKEKDVLMFRPTLNDGNTTQMLRNTT 120
 121 YCSKVAPELEVVOQSCFNSPMKLPVHKLYIEYGIQRTCPNDVGYPSSVAPRTITWNG 180
 121 YCSKVAPELEVVOQSCFNSPMKLPVHKLYIEYGIQRTCPNDVGYPSSVAPRTITWNG 180
 181 CYKIONFNNVIEPEGNNLSFLIALISNNGNYTCVTPYPNGRTFHLTRTLTVKVGSSPKNA 240
 181 CYKIONFNNVIEPEGNNLSFLIALISNNGNYTCVTPYPNGRTFHLTRTLTVKVGSSPKNA 240

XX OS Homo sapiens.
 XX XX US6280955-B1.
 XX XX 28-AUG-2001.
 XX XX 16-DEC-1997; 97US-0991944.
 XX XX 16-DEC-1997; 97US-0991944.
 XX XX (TULAR-) TULARIK INC.
 XX XX Cao Z; *
 XX DR MPI: 2001-595441/67.
 XX N-PSDB; AAS15608.
 PT Isolated polypeptide designated interleukin receptor accessory
 PS polypeptide is useful for regulating cell function
 PS Disclosure; Page - ; 21pp; English.
 CC This sequence represents the human interleukin-1 receptor accessory
 CC protein (IL-1Racp) mutant delta C2 of the invention. This mutant
 CC was used to define domains of the IL-1Racp protein that have the
 CC ability to activate NF-kappaB expression. The interleukin receptor
 CC accessory protein (IL-1Racp) and its modulators (agonists/antagonists)
 CC are useful for regulating cell function. Transient expression of either
 CC IL-1RI or IL-1Racp alone does not result in ligand-independent induction
 CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
 CC coexpression of both proteins resulted in a 20-fold increase in
 CC activation of NF-kappaB activity to a level comparable to that induced
 CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as
 CC a result of protein overexpression can elicit a signaling pathway
 CC leading to NF-kappaB activation. Modulating signal transduction
 CC involving NF-kappaB in a cell may be achieved by modulating the activity
 CC of IL-1Racp using binding agents such as agonists and antagonists.
 CC Hybridisation probes to the cDNA sequence can be used to identify wild-
 CC type and mutant IL-1Racp alleles in clinical and laboratory
 CC samples. Mutant alleles are used to generate allele-specific
 CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
 CC of diseases or disorders with an inflammatory response. In
 CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
 CC cellular expression or intracellular concentration of available
 CC active IL-1Racp. This invention also comprises a method of screening for
 CC an agent that modulates the interaction of an interleukin receptor
 CC accessory polypeptide (IL-1Racp) to a binding target.
 CC Note: The present sequence is not included in the
 CC specification but was created from the human IL-1R ACP sequence
 CC appearing as AA09966 and the information given in table 1 of the
 CC specification.
 CC XX
 CC SQ Sequence 540 AA:
 Query Match 69.7%; Score 2559; DB 22; Length 540;
 Best Local Similarity 88.3%; Pred. No. 2-7e-210;
 Matches 481; Conservative 28; Mismatches 24; Indels 12; Gaps 4;
 QY 1 MTLWCVSLVYFGILQSDASERCDMDGLDTKQIQVFEDEPARIKCPFEHFLKENVST 60
 DB 1 MTLWCVSLVYFGILQSDASERCDMDGLDTKQIQVFEDEPARIKCPFEHFLKENVST 60
 QY 61 AHSAGLTILWYTRQDRDLSEPINRPLPENRISKEQDVAFRPPTLLNDGNTTQMLRNTT 120
 DB 61 AHSAGLTILWYTRQDRDLSEPINRPLPENRISKEQDVAFRPPTLLNDGNTTQMLRNTT 120
 QY 121 YCSKAFPLEVVOKSCFNSPKMLPVHXYIEYGIORICPNVDGFPSSVPTTTWVG 180
 DB 121 YCSKAFPLEVVOKSCFNSPKMLPVHXYIEYGIORICPNVDGFPSSVPTTTWVG 180
 QY 181 CYKIONFNNVIEGKNTLSPFLALISNNGNYTCVYTPENGRTFHLTRTLTVKVGSPKNA 240

DB 181 CYKIONFNNVIEGKNTLSPFLALISNNGNYTCVYTPENGRTFHLTRTLTVKVGSPKNA 240
 QY 241 VPPVTHSPNDHVVYKKEGSEELLIPCTVYFSLMDSRNEMWMTIDKKPDDITDVTINE 300
 DB 241 VPPVTHSPNDHVVYKKEGSEELLIPCTVYFSLMDSRNEMWMTIDKKPDDITDVTINE 300
 QY 301 SISHRTEDETRTQILSIKKVTSBDLKRSYVCHASAKGEVAKAKVKQVAPRYVEL 360
 DB 301 SISHRTEDETRTQILSIKKVTSBDLKRSYVCHASAKGEVAKAKVKQVAPRYVEL 360
 QY 361 ACGFATVLLVYLILVYVYVWLEWVLFYRAHFGDTETLLDGKEVDIYVSARNABEEEF 420
 DB 361 ACGFATVLLVYLILVYVYVWLEWVLFYRAHFGDTETLLDGKEVDIYVSARNABEEEF 420
 QY 421 VLLTLRGVLENGFYKLCIPRDSLPQNTVEAVDFIORSRMTVMSPDVTEKSI 480
 DB 421 VLLTLRGVLENGFYKLCIPRDSLPQNTVEAVDFIORSRMTVMSPDVTEKSI 480
 QY 481 LEFKGVNCONSIAK---LIVEYRPLEHPHPIQLKES---VSFVWKGKSKSG 533
 DB 481 LEFKAGL---ENMASRGINIVILVOYKAVKETK--VKELKKAQTVLTVIKWKGSKYPO 535
 QY 534 SKFWK 538
 DB 536 GRFWK 540
 RESULT 6
 AAU09980
 ID AAU09980 standard; Protein; 530 AA.
 AC AAU09980;
 DT 21-MAY-2002 (first entry)
 DE Human IL-1R ACP protein deletion mutant delta C3.
 XX IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;
 KW IL-1; IL-1RI; mutant; mutein; delta C; inflammatory response.
 OS Homo sapiens.
 XX US6280955-B1.
 XX 28-AUG-2001.
 XX 16-DEC-1997; 97US-0991944.
 XX 16-DEC-1997; 97US-0991944.
 XX (TULAR-) TULARIK INC.
 XX Cao Z;
 XX MPI: 2001-595441/67.
 XX N-PSDB; AAS15608.
 PT Isolated polypeptide designated interleukin receptor accessory
 PS polypeptide is useful for regulating cell function
 PS Disclosure; Page - ; 21pp; English.
 CC This sequence represents the human interleukin-1 receptor accessory
 CC protein (IL-1Racp) mutant delta C3 of the invention. This mutant
 CC was used to define domains of the IL-1Racp protein that have the
 CC ability to activate NF-kappaB expression. The interleukin receptor
 CC accessory protein (IL-1Racp) and its modulators (agonists/antagonists)
 CC are useful for regulating cell function. Transient expression of either
 CC IL-1RI or IL-1Racp alone does not result in ligand-independent induction
 CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
 CC coexpression of both proteins resulted in a 20-fold increase in
 CC activation of NF-kappaB activity to a level comparable to that induced
 CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as

CC a result of protein overexpression can elicit a signaling pathway
 CC leading to NF-kappaB activation. Modulating signal transduction
 CC involving NF-kappaB in a cell may be achieved by modulating the activity
 CC of IL-1Racp using binding agents such as agonists and antagonists.
 CC Hybridization probes to the cDNA sequence can be used to identify wild-
 CC type and mutant IL-1Racp alleles in clinical and laboratory
 CC samples. Mutant alleles are used to generate allele-specific
 CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
 CC of diseases or disorders with an inflammatory response. In
 CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
 CC cellular expression or intracellular concentration or availability of
 CC active IL-1Racp. This invention also comprises a method of screening for
 CC an agent that modulates the interaction of an interleukin receptor
 CC accessory polypeptide (IL-1Racp) to a binding target.
 CC Note: The present sequence is not included in the
 CC specification but was created from the human IL-1R ACP sequence
 CC appearing as AAU09966 and the information given in table 1 of the
 CC specification.

XX Sequence 530 AA;

Query Match 68.9%; Score 2527; DB 22; Length 530;
 Best Local Similarity 89.0%; Pred. No. 1,5e-207;
 Matches 476; Conservative 26; Mismatches 21; Indels 12; Gaps 4;

QY 1 MTLLMVCVSLFYGIILQSDASERCDMDGLDMROIOVEDEPARIKPLFEHFLKFNYSY 60
 DB 1 MTLLMVCVSLFYGIILQSDASERCDMDGLDMROIOVEDEPARIKPLFEHFLKFNYSY 60
 QY 61 AHSAGLTLIWMTRQDDLEEPINRLPENRISKEKOVLMRPPLTMDTGYTCLMANTT 120
 DB 61 AHSAGLTLIWMTRQDDLEEPINRLPENRISKEKOVLMRPPLTMDTGYTCLMANTT 120
 QY 121 YCSKVAPELLEVQKDSGFNSPMKLPVHKLTYEYGIQRTICPNVDGYPSSVKTITWYMG 180
 DB 121 YCSKVAPELLEVQKDSGFNSPMKLPVHKLTYEYGIQRTICPNVDGYPSSVKTITWYMG 180
 QY 181 CYKIQNFNNVPEGMNLSFLIALISNNNGNTCVVTPENGRTFHLITLVKVGSPKNA 240
 DB 181 CYKIQNFNNVPEGMNLSFLIALISNNNGNTCVVTPENGRTFHLITLVKVGSPKNA 240
 QY 241 VPPYIHSNDIVYVKEGEBELLIPCTVYFSPFLMSRNEVMTIDGKKPDITIDVTINE 300
 DB 241 VPPYIHSNDIVYVKEGEBELLIPCTVYFSPFLMSRNEVMTIDGKKPDITIDVTINE 300
 QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVQKVPARYVEL 360
 DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVQKVPARYVEL 360
 QY 361 ACGFATYLVVILVYVYVWLEWVLYRAHFGTDETLIDGKEYDLYVSARNAEEREF 420
 DB 361 ACGFATYLVVILVYVYVWLEWVLYRAHFGTDETLIDGKEYDLYVSARNAEEREF 420
 QY 421 VLLTLRGLVLEBFGKLCIFPRDLSLPGNTVEAVDFIORSRMIIVLSPPDYTEKISIM 480
 DB 421 VLLTLRGLVLEBFGKLCIFPRDLSLPGNTVEAVDFIORSRMIIVLSPPDYTEKISIM 480
 QY 481 LEFLGVNCONSIAK---LIVERPLEHPHGILOLKE---VSFVSKGEG 528
 DB 481 LEFLGVNCONSIAK---LIVERPLEHPHGILOLKE---VSFVSKGEG 528
 QY 481 LEFLGVNCONSIAK---LIVERPLEHPHGILOLKE---VSFVSKGEG 528
 DB 481 LEFLGVNCONSIAK---LIVERPLEHPHGILOLKE---VSFVSKGEG 528

RESULT 7

ID AAU09973 standard; Protein; 559 AA.

XX AAU09973;

XX 21-MAY-2002 (first entry)

XX Human IL-1R ACP protein deletion mutant delta N1.

XX IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;

KW IL-1; IL-1RI; mutant; mutein; delta N1; inflammatory response.
 XX Homo sapiens.
 OS US6280955-B1.
 XX 28-AUG-2001.
 PD 16-DEC-1997; 97US-0991944.
 PF 16-DEC-1997; 97US-0991944.
 XX 16-DEC-1997; 97US-0991944.
 PR (TUL-1) TULARIK INC.
 PA Cao Z;
 PI WPI; 2001-595441/67.
 DR N-PSDB; AAS15608.
 XX Isolated polypeptide designated interleukin receptor accessory
 PT polypeptide is useful for regulating cell function
 PS Disclosure; Page - ; 21pp; English.

CC This sequence represents the human interleukin-1 receptor accessory
 CC protein (IL-1Racp) mutant delta N1 of the invention. This mutant
 CC was used to define domains of the IL-1Racp protein that have the
 CC ability to activate NF-kappaB expression. The interleukin receptor
 CC accessory protein (IL-1Racp) and its modulators (agonists/antagonists)
 CC are useful for regulating cell function. Transient expression of either
 CC IL-1RI or IL-1Racp alone does not result in ligand-independent induction
 CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
 CC coexpression of both proteins resulted in a 20-fold increase in
 CC activation of NF-kappaB activity to a level comparable to that induced
 CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as
 CC a result of protein overexpression can elicit a signaling pathway
 CC leading to NF-kappaB activation. Modulating signal transduction
 CC involving NF-kappaB in a cell may be achieved by modulating the activity
 CC of IL-1Racp using binding agents such as agonists and antagonists.
 CC Hybridization probes to the cDNA sequence can be used to identify wild-
 CC type and mutant IL-1Racp alleles in clinical and laboratory
 CC samples. Mutant alleles are used to generate allele-specific
 CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
 CC of diseases or disorders with an inflammatory response. In
 CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
 CC cellular expression or intracellular concentration or availability of
 CC active IL-1Racp. This invention also comprises a method of screening for
 CC an agent that modulates the interaction of an interleukin receptor
 CC accessory polypeptide (IL-1Racp) to a binding target.
 CC Note: The present sequence is not included in the
 CC specification but was created from the human IL-1R ACP sequence
 CC appearing as AAU09966 and the information given in table 1 of the
 CC specification.

XX Sequence 559 AA;

Query Match 68.8%; Score 2525; DB 22; Length 559;
 Best Local Similarity 85.0%; Pred. No. 2,4e-207;
 Matches 477; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

QY 12 FYGIILQSDASERCDMDGLDMROIOVEDEPARIKPLFEHFLKFNYSYAHSAQTLTIWY 71
 DB 1 FYGIILQSDASERCDMDGLDMROIOVEDEPARIKPLFEHFLKFNYSYAHSAQTLTIWY 71
 QY 72 WTRQDRLEEPINRLPENRISKEKOVLMRPPLTMDTGYTCLMANTTCSKVAPELEV 131
 DB 72 WTRQDRLEEPINRLPENRISKEKOVLMRPPLTMDTGYTCLMANTTCSKVAPELEV 131
 QY 132 VQKDSGFNSPMKLPVHKLTYEYGIQRTICPNVDGYPSSVKTITWYMGCKYIONFNNVI 191
 DB 132 VQKDSGFNSPMKLPVHKLTYEYGIQRTICPNVDGYPSSVKTITWYMGCKYIONFNNVI 191
 QY 192 PEGMNLSEFLIALISNNNGNTCVVTPENGRTFHLITLVKVGSPKNAVPPYIHSNDH 251

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|||||
DB 181 PEGANISFLALISNNGNVCTVTPENGRTFHLTRTLTKVGVSPKNAVPVISHSPNDH 240
OY 252 VYVEKERGEBELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINESISHRTEDT 311
DB 241 VYVEKERGEBELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINESISHRTEDT 300
OY 312 RQOILSIKVTSEDLKRSYVCHARSAGKGEVAKAAKVKQKVPAPRYVELACGATVTLV 371
DB 301 RQOILSIKVTSEDLKRSYVCHARSAGKGEVAKAAKVKQKVPAPRYVELACGATVTLV 360
OY 372 VILIVVHYVWLEMLVLPYRAHFGTDETTIDGKEYDIYVSYARNAEERFVLTIRGVLEN 431
DB 361 VILIVVHYVWLEMLVLPYRAHFGTDETTIDGKEYDIYVSYARNAEERFVLTIRGVLEN 420
OY 432 EFGYKLCIFDRDSLPGQIVTDETLISFQKSRLLVLSPNVYLQGTALLLELAGL---E 477
DB 421 EFGYKLCIFDRDSLPGQIVTDETLISFQKSRLLVLSPNVYLQGTALLLELAGL---E 477
OY 492 SIATK----LIVVEYRPLEHPHGILOLKESS--VSFVWKGKSKSKSKFVWALRLAL 544
DB 478 NMASRGNINVILOYKAVKETR--VKELKRAKTVLTVIKKGRKSKYPOGRFVWQLOVAM 535
OY 545 PLRSLASGCMNESCSSQSDI 565
DB 536 PVKSPRRSSSDQGLSYSL 556

RESULT 8
AAU09987
ID AAU09987 standard; Protein; 512 AA.
XX AAU09987;
XX
XX 21-MAY-2002 (first entry)
DE Human IL-1R ACP protein deletion mutant delta C2 #2.
XX
XX IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;
XX IL-1; IL-1R1; mutant; mutein; delta C2; inflammatory response.
XX
XX Homo sapiens.
XX OS
XX US6280955-B1.
XX PN
XX 28-AUG-2001.
PF 16-DEC-1997; 97US-0991944.
XX
XX 16-DEC-1997; 97US-0991944.
XX
XX (TULA-) TULARIK INC.
XX
XX Cao Z;
XX
XX MPI; 2001-595441/67.
XX DR N-PSDB; AAS15608.
XX
XX Isolated polypeptide designated interleukin receptor accessory
XX PT polypeptide is useful for regulating cell function
XX
XX PS Disclosure; Page - ; 21pp; English.
XX
XX This sequence represents the human interleukin-1 receptor accessory
XX CC protein (IL-1Racp) mutant delta C2 #2 of the invention. This deletion
XX CC mutant was used to define a phosphorylated domain of the IL-1Racp
XX CC protein at tyrosine 503. The interleukin receptor accessory protein
XX CC (IL-1Racp) and its modulators (agonists/antagonists) are useful
XX CC for regulating cell function. Transient expression of either IL-1R1
XX CC or IL-1Racp alone does not result in ligand-independent induction
XX CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
XX CC coexpression of both proteins resulted in a 20-fold increase in
XX CC activation of NF-kappaB activity to a level comparable to that induced

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CC by IL-1. These data suggest that aggregation of IL-1R1 and IL-1Racp as
CC a result of protein overexpression can elicit a signaling pathway
CC leading to NF-kappaB activation. Modulating signal transduction
CC involving NF-kappaB in a cell may be achieved by modulating the activity
CC of IL-1Racp using binding agents such as agonists and antagonists.
CC Hybridisation probes to the cDNA sequence can be used to identify wild-
CC type and mutant IL-1Racp alleles in clinical and laboratory
CC samples. Mutant alleles are used to generate allele-specific
CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
CC of diseases or disorders with an inflammatory response. In
CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
CC cellular expression or intracellular concentration or availability of
CC active IL-1Racp. This invention also comprises a method of screening for
CC an agent that modulates the interaction of an interleukin receptor
CC accessory polypeptide (IL-1Racp) to a binding target.
CC Note: The present sequence is not included in the
CC specification but was created from the human IL-1R ACP sequence
CC appearing as AAU09966 and the information given in table 1 of the
CC specification.
XX
XX Sequence 512 AA;
SQ
Query Match 68.2%; Score 2502.5; DB 22; Length 512;
Best Local Similarity 92.0%; Pred. No. 1.7e-205;
Matches 469; Conservative 20; Mismatches 14; Indels 7; Gaps 2;
OY 1 MTLKMCVSLYFYGILOSDBSRCDMGDITWMOIOVFEDEPARIKCPLEHEFLAKENYST 60
DB 1 MTLKMCVSLYFYGILOSDBSRCDMGDITWMOIOVFEDEPARIKCPLEHEFLAKENYST 60
OY 61 AHSAGLTLIWMYTRQDRDLSEPINFLPENRISKEDVLMFRFTLLANDTGYTCMLRNTT 120
DB 61 AHSAGLTLIWMYTRQDRDLSEPINFLPENRISKEDVLMFRFTLLANDTGYTCMLRNTT 120
OY 121 YCSKVAFPLEVOGKSCFNSPMLPVPKLYIEGIQRTCPNDGYPSSVKPTITWYMG 180
DB 121 YCSKVAFPLEVOGKSCFNSPMLPVPKLYIEGIQRTCPNDGYPSSVKPTITWYMG 180
OY 181 CYKIONNNVPIPGMNLSPFLALISNNGNVCTVTPENGRTFHLTRTLTKVGVSPKNA 240
DB 181 CYKIONNNVPIPGMNLSPFLALISNNGNVCTVTPENGRTFHLTRTLTKVGVSPKNA 240
OY 241 VPEVIHSPNDHVYVEKERGEBELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
DB 241 VPEVIHSPNDHVYVEKERGEBELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
OY 301 SISHSRTEDTRQOILSIKVTSEDLKRSYVCHARSAGKGEVAKAAKVKQKVPAPRYVEL 360
DB 301 SISHSRTEDTRQOILSIKVTSEDLKRSYVCHARSAGKGEVAKAAKVKQKVPAPRYVEL 360
OY 361 ACGFGATVLLVLLIVVHYVWLEMLVLPYRAHFGTDETTIDGKEYDIYVSYARNAEERF 420
DB 361 ACGFGATVLLVLLIVVHYVWLEMLVLPYRAHFGTDETTIDGKEYDIYVSYARNAEERF 420
OY 421 VLLTRGVLENRGYKLCIFDRDSLPGQIVTDETLISFQKSRLLVLSPNVYLQGTALL 480
DB 421 VLLTRGVLENRGYKLCIFDRDSLPGQIVTDETLISFQKSRLLVLSPNVYLQGTALL 480
OY 481 LBEFGVGMCONSIA TK---LIVVEYRPLE 506
DB 481 LELKAGL---ENMASRGNINVILOYKAVK 507

RESULT 9
AAU09981
ID AAU09981 standard; Protein; 520 AA.
XX AAU09981;
XX
XX 21-MAY-2002 (first entry)
DE Human IL-1R ACP protein deletion mutant delta C4.
XX

```


XX Example 7; Page 78-80; 115pp; English.

PS Mouse interleukin-1 receptor accessory protein (IL-1R ACP) (AA001913)
 CC is a protein that inhibits the ability of IL-1 to bind to, or
 CC otherwise activate, the IL-1R, esp. the Type 1 IL-1R. Its amino
 CC acid sequence was deduced from a cDNA clone (AA032028) derived
 CC from 3R3-IL cells. A human homologue (AA001911) of the IL-1R ACP
 CC has been isolated that is useful in modulating the inflammatory
 CC and immunological activities of human IL-1.

XX Sequence 570 AA;

Query Match 63.4%; Score 2327.5; DB 17; Length 570;
 Best Local Similarity 75.9%; Pred. No. 2e-190;
 Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

1 MTLWCVSLVYFGILQSDASERCDMDGIDTMROIQVEDEPARIKCPLFEHFLKFNST 60
 1 MGLMTYMSLSFGILQSHASERCDMDGIDTMROIQVEDEPARIKCPLFEHFLKFNST 60
 61 AHSAGTLIWTWTRQDRDLSEEPINFRLEPNRISKEDVLMFRPTLNDGNTQMLRNTT 120
 61 AHSAGTLIWTWTRQDRDLSEEPINFRLEPNRISKEDVLMFRPTLNDGNTQMLRNTT 120
 121 YCSKVAFLVAVVQKSCFNSPMKLPHKLYIEGRIQITCPNVGDFPSSVAPSTWTKG 180
 121 YCSKVAFLVAVVQKSCFNSPMKLPHKLYIEGRIQITCPNVGDFPSSVAPSTWTKG 180
 181 CYKIONFNNVPIEGMNLSTLALISNNNGYTCVVTYPENGRFHLTRTLTVKVGSPKNA 240
 181 CTEIVDFHNVLPBGMLSPFIPVSNNGYTCVVTYPENGRFHLTRTLTVKVGSPKNA 240
 241 VPPVHSPNDVHYEKEGEBELIPCTVYFSLMDSRNEVMTIDGKDDITDVTINE 300
 241 LPQIYSPNDRVYKEGEBELIPCKYVFSFIMDSHNEVMTIDGKDDITDVTINE 300
 301 SISHRTEDERTQILSIKKTSEDLSKSYCHASAKGEVAKAAXKQKVPARYTEL 360
 301 SVSYSTEDERTQILSIKKTSEDLSKSYCHASAKGEVAKAAXKQKVPARYTEL 360
 361 ACGFATVLLVYLIVVHYVLEWLVFRAHGTDETLIDGEXDIYVSARNAEEEF 420
 361 ACGFATVLLVYLIVVHYVLEWLVFRAHGTDETLIDGEXDIYVSARNAEEEF 420
 421 VLLTRGVLENERGYLCTIPDRDSLPGNTVEAVDFIORSRMATVLSPDVTEKSISM 480
 421 VLLTRGVLENERGYLCTIPDRDSLPGNTVEAVDFIORSRMATVLSPDVTEKSISM 480
 481 LEPKGVGMGQNSIATK---LIVVEYRPLEHHPHGLQKES---VSFVSWGKSKHSG 533
 481 LELKAGL--ENNASGNINVLIVQKAVKDK--VKEILRAKTVLTVIKMGKSKYPO 535
 534 SKFWKRLALPLRLSLASSGNIES 558
 536 GRFWKQLQVAMPVK---SPRMSN 557

RESULT 11
 ID AAU09967 standard; Protein; 570 AA.
 AC AAU09967;
 XX 21-MAY-2002 (first entry)
 DT Mouse interleukin-1 Receptor accessory protein (IL-1R ACP) protein.
 XX Mouse interleukin-1 Receptor accessory protein (IL-1R ACP) protein.
 DE IL-1R ACP; mouse; interleukin-1 receptor accessory protein; NF-kappaB;
 KM IL-1; IL-1R; inflammatory response.
 XX Mus sp.
 OS

PN US6280955-B1.
 XX 28-AUG-2001.
 PD 16-DEC-1997; 97US-0991944.
 XX 16-DEC-1997; 97US-0991944.
 PF 16-DEC-1997; 97US-0991944.
 XX (TULA-) TULARIK INC.
 PA Cao Z;
 XX WPI; 2001-595441/67.
 DR N-P8DB; AAS15609.
 XX Isolated polypeptide designated interleukin receptor accessory
 PT polypeptide is useful for regulating cell function
 PS Disclosure; Fig 1; 21pp; English.

This sequence represents the mouse interleukin-1 receptor accessory protein (IL-1R ACP), the cDNA sequence for this protein was used to generate a hybridisation probe that was used to isolate the human IL-1R ACP cDNA sequence of the invention. The interleukin-1 receptor accessory protein (IL-1R ACP) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either IL-1R1 or IL-1R ACP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-1R1 and IL-1R ACP as a result of protein overexpression can elicit a signaling pathway leading to NF-kappaB activation. Modulating signal transduction involving NF-kappaB in a cell may be achieved by modulating the activity of IL-1R ACP using binding agents such as agonists and antagonists. Hybridisation probes to the cDNA sequence can be used to identify wild-type and mutant IL-1R ACP alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In therapy, therapeutic IL-1R ACP nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active IL-1R ACP. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor accessory polypeptide (IL-1R ACP) to a binding target.

Sequence 570 AA;
 Query Match 63.4%; Score 2327.5; DB 22; Length 570;
 Best Local Similarity 75.9%; Pred. No. 2e-190;
 Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

1 MTLWCVSLVYFGILQSDASERCDMDGIDTMROIQVEDEPARIKCPLFEHFLKFNST 60
 1 MGLMTYMSLSFGILQSHASERCDMDGIDTMROIQVEDEPARIKCPLFEHFLKFNST 60
 61 AHSAGTLIWTWTRQDRDLSEEPINFRLEPNRISKEDVLMFRPTLNDGNTQMLRNTT 120
 61 AHSAGTLIWTWTRQDRDLSEEPINFRLEPNRISKEDVLMFRPTLNDGNTQMLRNTT 120
 121 YCSKVAFLVAVVQKSCFNSPMKLPHKLYIEGRIQITCPNVGDFPSSVAPSTWTKG 180
 121 YCSKVAFLVAVVQKSCFNSPMKLPHKLYIEGRIQITCPNVGDFPSSVAPSTWTKG 180
 181 CYKIONFNNVPIEGMNLSTLALISNNNGYTCVVTYPENGRFHLTRTLTVKVGSPKNA 240
 181 CTEIVDFHNVLPBGMLSPFIPVSNNGYTCVVTYPENGRFHLTRTLTVKVGSPKNA 240
 241 VPPVHSPNDVHYEKEGEBELIPCTVYFSLMDSRNEVMTIDGKDDITDVTINE 300
 241 LPQIYSPNDRVYKEGEBELIPCKYVFSFIMDSHNEVMTIDGKDDITDVTINE 300
 301 SISHRTEDERTQILSIKKTSEDLSKSYCHASAKGEVAKAAXKQKVPARYTEL 360

XX 16-DEC-1997; 97US-0991944.
 XX (TULAR-) TULARIK INC.
 XX Cao Z;
 XX WPI; 2001-595441/67.
 DR N-PSDB; AAS15608.
 XX
 PT Isolated polypeptide designated interleukin receptor accessory
 PT polypeptide is useful for regulating cell function
 PS
 XX Disclosure; Page - ; 21pp; English.
 CC This sequence represents the human interleukin-1 receptor accessory
 CC protein (IL-1Racp) mutant delta N2 of the invention. This mutant
 CC was used to define domains of the IL-1Racp protein that have the
 CC ability to activate NF-kappaB expression. The interleukin receptor
 CC accessory protein (IL-1Racp) and its modulators (agonists/antagonists)
 CC are useful for regulating cell function. Transient expression of either
 CC IL-1RI or IL-1Racp alone does not result in ligand-independent induction
 CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
 CC coexpression of both proteins resulted in a 20-fold increase in
 CC activation of NF-kappaB activity to a level comparable to that induced
 CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as
 CC a result of protein overexpression can elicit a signaling pathway
 CC involving NF-kappaB activation. Modulating signal transduction
 CC involving NF-kappaB in a cell may be achieved by modulating the activity
 CC of IL-1Racp using binding agents such as agonists and antagonists.
 CC Hybridization probes to the cDNA sequence can be used to identify wild-
 CC type and mutant IL-1Racp alleles in clinical and laboratory
 CC samples. Mutant alleles are used to generate allele-specific
 CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
 CC of diseases or disorders with an inflammatory response. In
 CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
 CC cellular expression or intracellular concentration or availability of
 CC active IL-1Racp. This invention also comprises a method of screening for
 CC an agent that modulates the interaction of an interleukin receptor
 CC accessory polypeptide (IL-1Racp) to a binding target.
 CC Note: The present sequence is not included in the
 CC specification but was created from the human IL-1R ACP sequence
 CC appearing as AAU09966 and the information given in table 1 of the
 CC specification.
 CC
 CC Sequence 508 AA;
 CC
 CC Query Match 61.1%; Score 2243; DB 22; Length 508;
 CC Best Local Similarity 83.5%; Pred. No. 3e-183;
 CC Matches 426; Conservative 35; Mismatches 37; Indels 12; Gaps 4;
 CC
 CC QY 63 SAGLTLLIYWTRODRDLEBPINFLPENRISKEKDVLMFRPTLLNDTGNVTCMLRNTTTC 122
 CC DB 1 SAGLTLLIYWTRODRDLEBPINFLPENRISKEKDVLMFRPTLLNDTGNVTCMLRNTTTC 60
 CC QY 123 SKAARFLEVOQKSCFSPMKLPVHKIYIEGIRITCPNDVGPSSVYRTTWGCV 182
 CC DB 61 SKAARFLEVOQKSCFSPMKLPVHKIYIEGIRITCPNDVGPSSVYRTTWGCV 120
 CC QY 183 KIQNFNNVIEGNNLSTFLIALISNNNGNTCVATYPENGRFTHLRRITLVKVGSPKAAVP 242
 CC DB 121 KIQNFNNVIEGNNLSTFLIALISNNNGNTCVATYPENGRFTHLRRITLVKVGSPKAAVP 180
 CC QY 243 PVTHSPNDHVVYKEPEBELLPCTVYFSFLMDSRNEVMTITDKKDDITITVTINEST 302
 CC DB 181 PVTHSPNDHVVYKEPEBELLPCTVYFSFLMDSRNEVMTITDKKDDITITVTINEST 240
 CC QY 303 SHSTEDTETRTQLISTIKVTSEDLKRSVCHABSAKGVAAAKVAKVAPRTVYLAC 362
 CC DB 241 SHSTEDTETRTQLISTIKVTSEDLKRSVCHABSAKGVAAAKVAKVAPRTVYLAC 300
 CC QY 363 GFGATVLLVVLIVVYVYVLMVLFYRAHGTBETLIDGKEYDIYVSANNAEERFVL 422

DB 301 GFGATVLLVVLIVVYVYVLMVLFYRAHGTBETLIDGKEYDIYVSANNAEERFVL 360
 QY 423 LTLRGVLENEFGYKLCIFPRDSIPGNTVEAVDFIORSRMIIVLSPDYTEKSISMLE 482
 DB 361 LTLRGVLENEFGYKLCIFPRDSIPGNTVEAVDFIORSRMIIVLSPDYTEKSISMLE 420
 QY 483 PKLGVNCONSIAIK---LIVVEYRPLEHPHPIIQLKES---VSFVSKGEKSKISGSK 535
 DB 421 LKAGL---ENMASRGNINVLIVQYKAVETK--VKELKRAKTVLTVIKWGEKSKYPOGR 475
 QY 536 FWKALRLALPLSLASGMSGSCSSQSDI 565
 DB 476 FWKQLQVAMPVKKSPRRSSDEGLSYSL 505
 CC
 CC RESULT 14
 CC AAU09982
 CC ID AAU09982 standard; Protein; 501 AA.
 CC XX
 CC AC AAU09982;
 CC XX
 CC DT 21-MAY-2002 (first entry)
 CC XX
 CC DE Human IL-1R ACP protein deletion mutant delta N1 #2.
 CC XX
 CC KW IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;
 CC IL-1; IL-1RI; mutant; mutein; delta N1; inflammatory response.
 CC OS Homo sapiens.
 CC XX
 CC PN US6280955-B1.
 CC XX
 CC PD 28-AUG-2001.
 CC XX
 CC PF 16-DEC-1997; 97US-0991944.
 CC XX
 CC PR 16-DEC-1997; 97US-0991944.
 CC XX
 CC PA (TULAR-) TULARIK INC.
 CC PI Cao Z;
 CC WPI; 2001-595441/67.
 CC DR N-PSDB; AAS15608.
 CC XX
 CC PT Isolated polypeptide designated interleukin receptor accessory
 CC polypeptide is useful for regulating cell function
 CC PS
 CC Disclosure; Page - ; 21pp; English.
 CC
 CC This sequence represents the human interleukin-1 receptor accessory
 CC protein (IL-1Racp) mutant delta N1 #2 of the invention. This deletion
 CC mutant was used to define a phosphorylated domain of the IL-1Racp
 CC protein at tyrosine 503. The interleukin receptor accessory protein
 CC (IL-1Racp) and its modulators (agonists/antagonists) are useful
 CC for regulating cell function. Transient expression of either IL-1RI
 CC or IL-1Racp alone does not result in ligand-independent induction
 CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
 CC coexpression of both proteins resulted in a 20-fold increase in
 CC activation of NF-kappaB activity to a level comparable to that induced
 CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as
 CC a result of protein overexpression can elicit a signaling pathway
 CC leading to NF-kappaB activation. Modulating signal transduction
 CC involving NF-kappaB in a cell may be achieved by modulating the activity
 CC of IL-1Racp using binding agents such as agonists and antagonists.
 CC Hybridization probes to the cDNA sequence can be used to identify wild-
 CC type and mutant IL-1Racp alleles in clinical and laboratory
 CC samples. Mutant alleles are used to generate allele-specific
 CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
 CC of diseases or disorders with an inflammatory response. In
 CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
 CC cellular expression or intracellular concentration or availability of
 CC active IL-1Racp. This invention also comprises a method of screening for

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:51:01 ; Search time 30 Seconds
(Without alignments)
673.785 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669
Sequence: 1 MTLWCVSLYFYGLQSDA.....SALALHFTDLSNNDFYIL 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ached: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgml2_6/prodata/1/aa/5A COMB .pep.*
- 2: /cgml2_6/prodata/1/aa/5B COMB .pep.*
- 3: /cgml2_6/prodata/1/aa/6A COMB .pep.*
- 4: /cgml2_6/prodata/1/aa/6B COMB .pep.*
- 5: /cgml2_6/prodata/1/aa/PCTUS COMB .pep.*
- 6: /cgml2_6/prodata/1/aa/backfile1 .pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2586	70.5	570	4	US-08-991-944-2
2	2586	70.5	570	4	US-09-173-151A-36
3	2327.5	63.4	570	4	US-08-991-944-4
4	2327.5	63.4	570	4	US-09-173-151A-21
5	825	22.5	579	4	US-09-173-151A-2
6	800	21.8	579	4	US-09-173-151A-2
7	762.5	20.8	579	4	US-09-173-151A-35
8	528	14.4	541	3	US-08-604-333-2
9	528	14.4	541	3	US-09-110-618-2
10	528	14.4	541	4	US-09-173-151A-28
11	520	14.2	521	3	US-09-578-178-2
12	520	14.2	521	3	US-08-996-338-20
13	496	13.5	555	1	US-09-173-151A-32
14	484.5	13.2	576	1	US-07-821-716-4
15	484.5	13.2	576	2	US-08-381-603-4
16	484.5	13.2	576	4	US-08-924-376-4
17	484.5	13.2	576	4	US-08-685-212-4
18	484.5	13.2	576	4	US-09-173-151A-30
19	484.5	13.2	576	4	US-08-466-932A-4
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21	484.5	13.2	576	5	PCT-US96-08899-4
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23	479	13.1	537	3	US-09-110-618-4
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25	479	13.1	537	4	US-09-578-178-4
26	478	13.0	519	3	US-08-996-338-21
27	478	13.0	567	4	US-09-560-639-7

28	478	13.0	567	4	US-09-173-151A-24	Sequence 24, Appl
29	478	13.0	567	4	US-09-032-337-39	Sequence 39, Appl
30	471.5	12.9	599	4	US-09-173-151A-10	Sequence 10, Appl
31	463.5	12.6	556	4	US-09-560-639-8	Sequence 8, Appl
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33	457	12.5	561	4	US-09-173-151A-23	Sequence 23, Appl
34	446	12.2	614	4	US-09-173-151A-16	Sequence 16, Appl
35	445	12.1	562	4	US-09-227-717-2	Sequence 2, Appl
36	444.5	12.1	562	4	US-09-173-151A-14	Sequence 14, Appl
37	444.5	12.1	562	4	US-09-227-717-2	Sequence 22, Appl
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41	424.5	11.6	569	4	US-08-924-376-2	Sequence 2, Appl
42	424.5	11.6	569	4	US-08-685-212-2	Sequence 2, Appl
43	424.5	11.6	569	4	US-09-173-151A-31	Sequence 31, Appl
44	424.5	11.6	569	4	US-08-466-932A-2	Sequence 2, Appl
45	424.5	11.6	569	5	PCT-US94-02414-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-991-944-2

Sequence 2, Application US/08991944
Patent No. 6280955

GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan

TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
TITLE OF INVENTION: Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH
STATE: CALIFORNIA

COUNTRY: USA
ZIP: 94010

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/991,944
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-014
TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 570 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-991-944-2

Query Match 70.5%; Score 2586; DB 4; Length 570;
Best Local Similarity 85.3%; Pred. No. 2.8e-244;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

QY 1 MTLWCVSLYFYGLQSDASERCDWGLTMOIOVFEDPARIKCPLEHFKRYST 60
DB 1 MTLWCVSLYFYGLQSDASERCDWGLTMOIOVFEDPARIKCPLEHFKRYST 60
QY 61 AHSAGLTLLIYWTRODRLDEPIINFLLPENRISKQDVLFRRPTLLANDTGYTCLMANTT 120

Thu May 1 09:36:18 2003

us-10-061-727-2.ra1

Page 2

Db 61 AHSAGLTLIWMYTRQDRDLEBPINFLPENRISKEKDVLMFRPTLLNDNGNTCMLRNTT 120
Qy 121 YGSKVAFPLEVQKSCFNSPKMLPVHKLXIYEGIORICPNVDGYPRSSVKTITWYMG 180
Db 121 YGSKVAFPLEVQKSCFNSPKMLPVHKLXIYEGIORICPNVDGYPRSSVKTITWYMG 180
Qy 181 CYKIQFNPNVIEPGNMLSLFLIALISNNGNTCVVTPENGRTFHLTRLTVKVGSPKNA 240
Db 181 CYKIQFNPNVIEPGNMLSLFLIALISNNGNTCVVTPENGRTFHLTRLTVKVGSPKNA 240
Qy 241 VPPVHSPNDHVVYEKEPGEELLIPCTVYFSLMDSRNEVMTIDGKEDDITIDVTINE 300
Db 241 VPPVHSPNDHVVYEKEPGEELLIPCTVYFSLMDSRNEVMTIDGKEDDITIDVTINE 300
Qy 301 SISHSTEDETRQIILSIKKTYSDDLKRSYVCHASAKGVAAKVKOKVAPRYTVEL 360
Db 301 SISHSTEDETRQIILSIKKTYSDDLKRSYVCHASAKGVAAKVKOKVAPRYTVEL 360
Qy 361 ACFGFATVLLVLLIVVHYVWLEWVLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
Db 361 ACFGFATVLLVLLIVVHYVWLEWVLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
Qy 421 VLLTTRGVLENERGYKLCIFDRDSLPGNTVEAVDFIORSRMIYVLSPDYVTEKSISM 480
Db 421 VLLTTRGVLENERGYKLCIFDRDSLPGNTVEAVDFIORSRMIYVLSPDYVTEKSISM 480
Qy 481 LERKLGVMCONSIATK---LIVVEYRPLEHPHGIOLKES--VSFVSMKGEKSKYHG 533
Db 481 LERKLGVMCONSIATK---LIVVEYRPLEHPHGIOLKES--VSFVSMKGEKSKYHG 533
Qy 534 SKFWKALRLALPLRLSLASGNNESCSQSDI 565
Db 534 GRFWKQLQVAMPVKSPRRSSDDEGLSYSSL 567

RESULT 2

US-09-173-151A-36
Sequence 36, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debers, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-173-151A-36

Query Match 70.5% Score 2586; DB 4; Length 570;

Best Local Similarity 85.3% Pred. No. 2.8e-244; Indels 12; Gaps 4;

Matches 488; Conservative 35; Mismatches 37;

Qy 1 MTLMLCVSLVYFYGILQSDASERCDDWGLDTRQIOVFEBEPARIKCPLFEHFLKFNYS 60
Db 1 MTLMLCVSLVYFYGILQSDASERCDDWGLDTRQIOVFEBEPARIKCPLFEHFLKFNYS 60
Qy 61 AHSAGLTLIWMYTRQDRDLEBPINFLPENRISKEKDVLMFRPTLLNDNGNTCMLRNTT 120
Db 61 AHSAGLTLIWMYTRQDRDLEBPINFLPENRISKEKDVLMFRPTLLNDNGNTCMLRNTT 120
Qy 121 YGSKVAFPLEVQKSCFNSPKMLPVHKLXIYEGIORICPNVDGYPRSSVKTITWYMG 180
Db 121 YGSKVAFPLEVQKSCFNSPKMLPVHKLXIYEGIORICPNVDGYPRSSVKTITWYMG 180
Qy 181 CYKIQFNPNVIEPGNMLSLFLIALISNNGNTCVVTPENGRTFHLTRLTVKVGSPKNA 240
Db 181 CYKIQFNPNVIEPGNMLSLFLIALISNNGNTCVVTPENGRTFHLTRLTVKVGSPKNA 240
Qy 241 VPPVHSPNDHVVYEKEPGEELLIPCTVYFSLMDSRNEVMTIDGKEDDITIDVTINE 300
Db 241 VPPVHSPNDHVVYEKEPGEELLIPCTVYFSLMDSRNEVMTIDGKEDDITIDVTINE 300
Qy 301 SISHSTEDETRQIILSIKKTYSDDLKRSYVCHASAKGVAAKVKOKVAPRYTVEL 360
Db 301 SISHSTEDETRQIILSIKKTYSDDLKRSYVCHASAKGVAAKVKOKVAPRYTVEL 360
Qy 361 ACFGFATVLLVLLIVVHYVWLEWVLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
Db 361 ACFGFATVLLVLLIVVHYVWLEWVLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
Qy 421 VLLTTRGVLENERGYKLCIFDRDSLPGNTVEAVDFIORSRMIYVLSPDYVTEKSISM 480
Db 421 VLLTTRGVLENERGYKLCIFDRDSLPGNTVEAVDFIORSRMIYVLSPDYVTEKSISM 480
Qy 481 LERKLGVMCONSIATK---LIVVEYRPLEHPHGIOLKES--VSFVSMKGEKSKYHG 533
Db 481 LERKLGVMCONSIATK---LIVVEYRPLEHPHGIOLKES--VSFVSMKGEKSKYHG 533
Qy 534 SKFWKALRLALPLRLSLASGNNESCSQSDI 565
Db 534 GRFWKQLQVAMPVKSPRRSSDDEGLSYSSL 567

RESULT 3

US-08-991-944-4
Sequence 4, Application US/08991944

Patent No. 6280955
GENERAL INFORMATION:
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
TITLE OF INVENTION: Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,944
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-014
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-991-944-4

Query Match 63.4%; Score 2327.5; DB 4; Length 570;
Best Local Similarity 75.9%; Pred. No. 5.7e-219;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

QY 1 MTLIMCVSLVYFGILSDASERCDDMDLDTMROIOVEDEBPARIKCLFHHFLKFNST 60
1 MGLIMVMSLSFYGLISHASERCDDMDLDMROIOVEDEBPARIKCLFHHFLKFNST 60
61 AHSAGLTIWYTRDODRDLPEPINFRLPENRISKEKDVLMFRPTLNDTGYTCMLRNTT 120
61 AHSAGLTIWYTRDODRDLPEPINFRLPENRISKEKDVLMFRPTLNDTGYTCMLRNTT 120
121 YCSFVAPFLVAVKOSCFNSPMKLPHKLYIEYGIQRTCPNVGYPSSVKPITTWYMG 180
121 YCSFVAPFLVAVKOSCFNSPMKLPHKLYIEYGIQRTCPNVGYPSSVKPITTWYMG 180
121 YCSFVAPFLVAVKOSCFNSPMKLPHKLYIEYGIQRTCPNVGYPSSVKPITTWYMG 180
181 CYKIONFNANVPEGMNLSFLALISNNGNATCVVTPYENGRTFHLTRLTIVKVVGPSNA 240
181 CTBLVDFFNANVPEGMNLSFLALISNNGNATCVVTPYENGRTFHLTRLTIVKVVGPSNA 240
241 VPPVTHSPNDHNVYKEKEBELLPCTVYFSPFLMDSRNEVMTIDGKKPDITDVTINE 300
241 LPQIYSPNDHNVYKEKEBELLPCTVYFSPFLMDSRNEVMTIDGKKPDITDVTINE 300
301 SISHSRTEDERTOLISIKKTSYEDIKRSYVCHASAKGEVAKAKVOKVAPRYTVEL 360
301 SISHSRTEDERTOLISIKKTSYEDIKRSYVCHASAKGEVAKAKVOKVAPRYTVEL 360
301 SVSSTSTEDERTOLISIKKTSYEDIKRSYVCHASAKGEVAKAKVOKVAPRYTVEL 360
361 ACGRGATVLLVILIVVHYVAVLEAVLFYRAHFGTDETLIDGKEVDIVSARNAEBSF 420
361 ACGRGATVLLVILIVVHYVAVLEAVLFYRAHFGTDETLIDGKEVDIVSARNAEBSF 420
421 VLLTRGVLENEFGYKLCIFRDSIPGNTVAVFPIQSRNMI VLSLSPDYTERKISM 480
421 VLLTRGVLENEFGYKLCIFRDSIPGNTVAVFPIQSRNMI VLSLSPDYTERKISM 480

QY 481 LEFKGVMCNSIATK----LIVVEYRLEPHPHGILQLES---VSPVSKGKGRSG 533
481 LEFKGVMCNSIATK----LIVVEYRLEPHPHGILQLES---VSPVSKGKGRSG 533
481 LEFKGVMCNSIATK----LIVVEYRLEPHPHGILQLES---VSPVSKGKGRSG 533
QY 534 SKFWKALRLALPLKSLASAGNES 558
534 SKFWKALRLALPLKSLASAGNES 558
536 GRFWKOLQVAMPVK--SPRWSN 557

RESULT 4
US-09-173-151A-21
Sequence 21, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-173-151A-21

Query Match 63.4%; Score 2327.5; DB 4; Length 570;

Best Local Similarity 75.9%; Pred. No. 5,7e-219;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

```

QY 1 MTLIMCVSLFYFGLIGSDASERCDMDLPTMROIOVFEDEPARIKCPLEHFLKFNYSY 60
  1 MGLIMVSLSPFYGLIGSDASERCDMDLPTMROIOVFEDEPARIKCPLEHFLKFNYSY 60
QY 61 AHSAGLTLIWMTRQDDLEBPINFLPENRISKEKOVLMFRPLTLDNGTYTCLMNTT 120
  61 AHSAGLTLIWMTRQDDLEBPINFLPENRISKEKOVLMFRPLTLDNGTYTCLMNTT 120
QY 121 YCSKVAPELLEVQKDSCEFSNPMKLPVHKLXIEYGIORTCPNVGVGFSSVYKPTIYMYG 180
  121 YCSKVAPELLEVQKDSCEFSNPMKLPVHKLXIEYGIORTCPNVGVGFSSVYKPTIYMYG 180
QY 181 CYKIQNFNNVPIPEGANISFLIALISNNNGNTCVVTPYENGFTFHLTRTLVTKVGSPEKNA 240
  181 CTBIYDFHNVLPBEGWNLSFPIPLVSNNGNTCVVTPYENGFTFHLTRTLVTKVGSPEKNA 240
QY 241 VPPYIHSNDHVYKEKGEELLPCTVYFSLMDSRREVMWTTIDGKKPDVTDITINE 300
  241 LPQIYSPNDVYKEKGEELLPCTVYFSLMDSRREVMWTTIDGKKPDVTDITINE 300
QY 301 SISHSRTEDERTIOILSIKVTSEDLKRSYVCHARSAGEVAKAKVOKVAPARYVEL 360
  301 SVSYSTEDERTIOILSIKVTSEDLKRSYVCHARSAGEVAKAKVOKVAPARYVEL 360
QY 361 ACGFATVLLVLIIVVHYVWLEMLFYRAHFGTDETLIDKEVDIVSYARNAEBEEF 420
  361 ACGFATVLLVLIIVVHYVWLEMLFYRAHFGTDETLIDKEVDIVSYARNAEBEEF 420
QY 421 VLTILRGVLENERKYKCTIPRDSLPNGNTVEAFDFIQSRRLVLSPPVTEKLSM 480
  421 VLTILRGVLENERKYKCTIPRDSLPNGNTVEAFDFIQSRRLVLSPPVTEKLSM 480
QY 481 LEFLGVNCONSIAK----LIIVYRPLEHPHPIQLKES---VSFVSKEGSKSHSG 533
  481 LEFLGVNCONSIAK----LIIVYRPLEHPHPIQLKES---VSFVSKEGSKSHSG 533
QY 534 SKFKALRLALPLRLSLASSGMNS 558
  534 GRFKOLQVAMPVK---SPRWSSN 557
Db 536 GRFKOLQVAMPVK---SPRWSSN 557

RESULT 5
US-09-173-151A-4
; Sequence 4, Application US/09173151A
; Patent No. 6326472
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debeets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods.
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNA Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/173,151A
; FILING DATE: 14-OCT-1998
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
US-09-173-151A-4

Query Match 22.5%; Score 825; DB 4; Length 686;
Best Local Similarity 31.9%; Pred. No. 1e-71;
Matches 228; Conservative 106; Mismatches 244; Indels 136; Gaps 27;

QY 1 MTLIMCVSLFYFGLIGSDASERCDMDLPTMROIOVFEDEPARIKCPLEHFLKFNYSY 59
  1 MGLIMVSLSPFYGLIGSDASERCDMDLPTMROIOVFEDEPARIKCPLEHFLKFNYSY 59
QY 60 TAHSAGLTLIWMTRQDDLEBPINFLPENRISKEKOVLMFRPLTLDNGTYTCLMNTT 119
  60 TAHSAGLTLIWMTRQDDLEBPINFLPENRISKEKOVLMFRPLTLDNGTYTCLMNTT 119
QY 66 TAOSTGLRLMY--KXGDLBEPILF--SEVRKSKEDSIWHFSAKQDSGFTCYLRLS 121
  66 TAOSTGLRLMY--KXGDLBEPILF--SEVRKSKEDSIWHFSAKQDSGFTCYLRLS 121
QY 120 YCSKVAPELLEVQKDS--CEFSNPMKLPVHKLXIEYG---IORTCPNVGVGFSSVXP 173
  120 YCSKVAPELLEVQKDS--CEFSNPMKLPVHKLXIEYG---IORTCPNVGVGFSSVXP 173
QY 122 TYCMKVSMSLTVAENESGLCYNSRIR-----YLEKSEVTKRKEISCDDMDDEKKSQDEP 175
  122 TYCMKVSMSLTVAENESGLCYNSRIR-----YLEKSEVTKRKEISCDDMDDEKKSQDEP 175
QY 174 TITVMOCYKIQNFNNVPIPEGANISFLIALISNNNGNTCVVTPYENGFTFHLTRTLVTKV 233
  174 TITVMOCYKIQNFNNVPIPEGANISFLIALISNNNGNTCVVTPYENGFTFHLTRTLVTKV 233
QY 176 DVWYKECKPKMRSIIIOGNALLIOEVQEDGANYTELKY--BGKL--VARTTELKY 231
  176 DVWYKECKPKMRSIIIOGNALLIOEVQEDGANYTELKY--BGKL--VARTTELKY 231
QY 234 VGSFKNAVPPVLIHSPNDHVYKEKGEELLPCTVYFSLMDSRREVMWTTIDGKTPDDI 292
  234 VGSFKNAVPPVLIHSPNDHVYKEKGEELLPCTVYFSLMDSRREVMWTTIDGKTPDDI 292
QY 232 TALLTDGPPKPLFPMENQPSVIDVOLKPLNIPCKAFPGSSGSGMIYK--MKGEK---- 286
  232 TALLTDGPPKPLFPMENQPSVIDVOLKPLNIPCKAFPGSSGSGMIYK--MKGEK---- 286
QY 293 TIDVTINESISHSRTEDERT-----TQILSIKVTSEDLKRSYVCHARSAGEV 341
  293 TIDVTINESISHSRTEDERT-----TQILSIKVTSEDLKRSYVCHARSAGEV 341
QY 287 -----FIELAGHIR--BGEIRILKEHLGEKEVELALIFDSVEADL--ANYCHVENENGR- 339
  287 -----FIELAGHIR--BGEIRILKEHLGEKEVELALIFDSVEADL--ANYCHVENENGR- 339
QY 342 AKAKVYKQKVPARYVELAOCGATVLLVLIIVVHYVWLEMLFYRAHFGTDETLID 401
  342 AKAKVYKQKVPARYVELAOCGATVLLVLIIVVHYVWLEMLFYRAHFGTDETLID 401
QY 340 -KASVILRRKDDLIYKIELAGJGALIFLLVLIIVYKCNIEHMLPYHQHFGADETNDI 398
  340 -KASVILRRKDDLIYKIELAGJGALIFLLVLIIVYKCNIEHMLPYHQHFGADETNDI 398
QY 402 GKEYDIVSYAR-----NAEEEFVLLTRGLVLENEFGYKLCIFPRDSLPGGNTVE 452
  402 GKEYDIVSYAR-----NAEEEFVLLTRGLVLENEFGYKLCIFPRDSLPGGNTVE 452
QY 399 NKETDALISTTKVDQDPTLDCDNEBEQFALEVPDLVEKHGYKLCIIPERDLIPSGTYE 458
  399 NKETDALISTTKVDQDPTLDCDNEBEQFALEVPDLVEKHGYKLCIIPERDLIPSGTYE 458
QY 453 AVDFIQSRRLVLSPPVTEKLSISMLEFKGVNCONSIAK---KLIVYRPLEHPH 509
  453 AVDFIQSRRLVLSPPVTEKLSISMLEFKGVNCONSIAK---KLIVYRPLEHPH 509
QY 459 DLTRYVQSRRLIIVLIPDYILRRGWSI--FELESRLHMLVSGEIKVILLIECTELK--- 513
  459 DLTRYVQSRRLIIVLIPDYILRRGWSI--FELESRLHMLVSGEIKVILLIECTELK--- 513

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QY 510 PG-----ILQKESV---SFVSMGKESKHSKSKFKALRLALPLR----- 547
DB 514 -GKVNCOEVSLSKRSIKLSLIMKSSKSKSLNSKFKVHLVYEMPIKCKMELRCHVLDS 572
QY 548 -----SLSSSGMWNSSCSQSDISLDHVQRRSRUKPEPLOS----- 586
DB 573 AEQGLFGLQPIPSIMATSTATLVSQADL-----PEFPPSDMQIRHC 617
QY 587 -----ERAAGSPAPKMSKHSKKSATRCVCYCEGENHLRN--KSRAEIH 632
DB 618 CRGKHIEPATLPLVPSLGNH-----TYCNLPLTLNLGQLPLNLTIKQDQEFH 666

RESULT 6
US-09-173-151A-2
Sequence 2, Application US/09173151A
Patent No. 6326472

GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-173-151A-2
Query Match 21.8%; Score 800; DB 4; Length 579;
Best Local Similarity 35.1%; Pred. No. 2.1e-69;
Matches 207; Conservative 96; Mismatches 208; Indels 78; Gaps 24;

QY 1 MTLLCWSVSLYFYGLQSD--ASERCDDWGLDTMRQIQVEEPEPAKIKPLFEHLKPNY 58
DB 3 LTL--VSTMLTVSTSSPLSDGICIMSV--LKYVALAEPRVKALVYSYIRNY 59
QY 59 STAHSAGLTLIYWRQDRLEPINFRLPENRISKQDVLFRPTLNDNTYTMCLR 118
DB 60 STAQSTGLRLIMY--KNKGDLPEPIF--SEVRMSKEBDSIMFHAADADSGFYCVLNN 115
QY 119 TTYCSVNAFPLEVQKDS--CNSPMKLPVHLXYEY--IORITCNVDGYPPSSVK 172
DB 116 STYCMKVSMLTVVAENESLCTNSRIR-----YLEKSEVTRKELISCPMDPPKSDOE 169
QY 173 PITWYMGCYKIQNFNNVPIEGMNLSPILALISNNGNYCVVYTPENGRTFHLTRLTVK 232
DB 170 PDVWYKCECKPQKMSIITOKGNALLIOVQEDGNTYCELY--EGKL--VRRTELK 225
QY 233 VVGSPPKNAV--PVIHSPNDHVVYEKEPGEELLIPCTVYFSPIMDSRNEVWTTIDKKPD 291
DB 226 VTALLTDKPKPLFPENQPSVIDQKPLNIPCKAFPGFSGSGPMIYM--MKGEK-- 281
QY 292 ITIDVTINESISHRTEDTR-----TOLSTIKYTSBDUKSYVCHASAKGE 340
DB 282 -----FIEELAHIR--EGEIRILKHLGKEVELALIFDSVVEAL--ANTYCHVENRNR 334
QY 341 VAKAKVKQVAPRYVELACPGATVLLVILVHVHVLEWLPFRAHGTDETL 400
DB 335 --KASVLLRKODLYKILAGLAGLIFLLVLLVLYIKVILMLFRQHFGADETND 392
QY 401 DKEKYDIYVSAR-----NAEEBEFVLLTLEGLVNEBQYKLCIFDRSLPGNT 450
DB 393 DKREDAVLYTKVQDPLDCCNPEEBOFALFVLPDVLKHKYGLFIERDLISGSAY 452
QY 451 VNAVDFIORSRMIVVLSPDVYTEKISMLEFKICWMCNSIAT--KLIVVERPLEH 507
DB 453 MEDLTRVYEOSRLIIVLPDYILRRGWSI--FELSRILHNNLVGGEIVIIIECTELK 509
QY 508 PHRG-----ILQKESV---SFVSMGKESKHSKSKFKALRLALPLR 547
DB 510 ---GKVNCOEVSLSKRSIKLSLIMKSSKSKSLNSKFKVHLVYEMPIK 555

RESULT 7
US-09-173-151A-35
Sequence 35, Application US/09173151A
Patent No. 6326472

GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-173-151A-35

Query Match 20.8%; Score 762.5; DB 4; Length 668;
Best Local Similarity 29.7%; Pred. No. 1,3e-65;
Matches 204; Conservative 119; Mismatches 274; Indels 91; Gaps 21;

QY 24 CDDWGLDTRMROIOVFEDEPARIKPLFEHLKFNYSSTAHSAGLTLIYWTRQDRDLLEPT 83
DB 3 CTWMSID-IKKYQVLVGEPAVKAICALEFYGYRTMYSLAQSHLSIMMYKSSGPDPEEPI 61
QY 84 NFRLEPERISKEKDVLMFRPLTNDGNYTCMLNTYCSKVAPLEVVQKDS--CENSP 141
DB 62 AF--DGSRMKEEDSIWFRPLTLDSDGLYACVINNSTYCMKVSISLTVGENDTGLCNSK 119
QY 142 MKLPHVHLTYIEYG----IORTCPNVGYPSPSVKPTITWYMGCYKIQNFNNVPIEGMNL 197
DB 120 MK-----YFKELSKSKSKISCRDIEDFLPTEPELWYKERTKTPMRPSIYFKDYL 173
QY 198 SFLLALISNNGNNTCVVTPYENGRTFHLTRTLTVKVVGSPKNAVPIVHSPNDH--VVE 255
DB 174 LIREVREDIDIGNYCEKLY--GGEVVRRTTELVT---APLTDKPKLALYPMESKLTIQE 228
QY 256 KEBGEELLICTVYFESFLMSRNEVMTIIOCKRPDI-----TIIDTINESISHSHTED 309
DB 229 TQJLDSANLTCRAFGSGDVSPLIYMWKGEKFTIEDENRWESDIRI--LKEHLGEQ 285
QY 310 ETRTQILSIKVTSEDKRSYVCHARSAKGEVAKAKAVKQVAPARYTVELACFGATVL 369
DB 286 EVSISL-VDSVERGDL-GNYSCEVENGNR--RHASVILMKRELMTVELAGLGLAILL 341
QY 370 LVVLIVVHYVYLEMVLFTRAHFGTDETLIDGKEYDIYVSYAR-----NAEEEF 420
DB 342 LVLCLVITYKYCKEIMLFYRNHFGAEELDGDNDYDAVLSYTVKVDPDQWNOETGEERE 401
QY 421 VLLTRGLVLENEFGYKLCIPRDSLPGCNTVEAVFPIQSRBMIVLSPDYTKESISM 480
DB 402 ALLELPMLLEHNGYKLPIDRDLIPGTYYIEDVARKVDOSKRLIIVMTPTVYVRKQMSI 461
QY 481 LEFRLGVMCONSIAI--KLIVREYRPLEHPHGLIQLKE-----SVSEFVSMGEX 528

DB 462 --FELETRLRNNLVTEIGIKVILIECSELR-----GIMNYQVEVALKRTIKLLVTKHGPX 515
QY 529 SKHSGSKPKKALRLALPLR-----SLASGGMNBSGSSQSDISLD 568
DB 516 CNKLNSKFWKRLQYEMPFRIEPTTHEQALDVEEGPFEELQTVSAISMAAATSTALATA 575
QY 569 HVOR-----RSRLKEPPELQSSERRAAGSPAPGCMKSHKRGSSATCCVYCEGEN 621
DB 576 HPLKESTFNHTYHSQMRQKHRYRSYEDV--PPTGLPLTISIGNQHTYCNIPMTLNGOR 633
QY 622 HLNKSRAEIHQPOWETHLCRPQES 649
DB 634 PQTSSREQNPDEAHNTNSAILPLLPRET 661

RESULT 8

US-08-604-333-2
Sequence 2, Application US/08604333
Patent No. 5776731

GENERAL INFORMATION:

APPLICANT: Partec, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FEB-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-604-333-2

Query Match 14.4%; Score 528; DB 1; Length 541;
Best Local Similarity 30.0%; Pred. No. 8.2e-43;
Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

QY 4 LMCVSLVLYGILQSDASRCDDWGLDTR-IOVFEDEPARIK-CPLEHFLKFNYSSTA 61
DB 10 LMLVLIV-----STASG-----TSRPHITVEGEPFYIAKH-----SCSLA 46
QY 62 HSAGLTL-IWYTRQDRDLLEPINFRLPENRISKENDVLMFRPLTNDGNYTCMLRNTT 120
DB 47 HELETTTKSMYKSSGQEHVE-LNPR-SSRIALHDCVLEFMEVLELNDGSGYFFQMKNYT 104
QY 121 YCSKAFPLEVQ--KDSGFN-----SPMLPVHKLTYIEGIGRITCPNNDGYPSPSVKPT 174
DB 105 Q---KMKNLVIRNKHSGFTERQVYSKIVEVKPF-----QITEN--SYQTQVNST 152
QY 175 ITWYMGCYKIQNFNNVPIE-GNMLSFLLALISNNGNNTCVVTPYENGRTFHLTRTLTVKY 233

Db 153 -SLYKCKLLLENNKQPIKKAER-----EDQGYSSCVHFLHNGKLFNITKTNTIT 206
 Qy 234 VSPKNAVPVPHSPNDHYVEKEPEGELLICTVYFSLMDSRNEVMTIDGKDDIT 293
 Db 207 VEDRSNIVPVLGPKLNHVAVEL--GKNVRLNC-----SALNBEVDIYMMFGENGSDPN 260
 Qy 294 IDVTINESISHSTEDERT-----OILSIKVTSEDLKRSYVCHASAKGEVAKA 345
 Db 261 I-----HEEKEMRIMTPGKMHASKVLRLENIGESLNLVNYCTVASTGTDTKSF 311
 Qy 346 KVKOK-----VPAARYVELAGSGFATVLI---VLLIYVHYVYLMVLPYRAHGTDE 397
 Db 312 ILVRKADMDIPGHVFT-----RGMIIAVILVAVCLVTCVYRVDLVLFYRHLTERDE 367
 Qy 398 TILDGEYDIYVSAR-----NAEERFVLLTLRGVLENEFGKLCIFDRDSLPGANTVE 452
 Db 368 TLDGTYTAFVSLKECPRENEHTFAVEILPRVLEKHFGLKCFERDVVPGAAVD 427
 Qy 453 AVDFIORSRMIVLSPDYTEKSIISMLEFKL-GVMCONSIAATKLIIVYERPLHHPH-- 509
 Db 428 EIHSLIEKSRRLIIVLSKYSMSNEVYELSGIHEALVERKI--KIILIEFTVTDTFTL 485
 Qy 510 PGILOKESVSPVSKGSKSGSKGSKFKWALRLALPLRSL 549
 Db 486 POSTKLKSHRVLKWKADKSLSYNSRFWKLILYIMPAKTV 525

RESULT 9

US-09-110-618-2
 ; Sequence 2, Application US/09110618
 ; Patent No. 6090918
 ; GENERAL INFORMATION:
 ; APPLICANT: Parinet, Patricia et al.
 ; TITLE OF INVENTION: Receptor Designated 2P1
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/110,618
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/604,333
 ; FILING DATE: 21-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Anderson, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2619
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 541 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-110-618-2
 Query Match 14.4%; Score 528; DB 3; Length 541;
 Best Local Similarity 30.0%; Pred. No. 8.2e-43;

Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;
 Qy 4 LMCVSLYFEGYLIQSDASERCDWGLDTR--OIYFEDPARIK--CPLEHFLKNEYSTA 61
 Db 10 LMLVLSV-----STASC-----TSRPHITVEGSPFLKLC-----SCSLA 46
 Qy 62 HSAGLTL-IWYTRQDRDLPEPINFELPNRISKEKDVLMFPRLTLNDGTNYCMRLNTT 120
 Db 47 HEIETTKSMYSSGSGQEHVE--LNPR--SSRIALHDCVLEFMPVELNDGVSFYFQKNY 104
 Qy 121 YCSKNAFPLEVQ--KDSGFN-----SPMLPPIHAKYIEIGIQRICPNVDGFPSSVKT 174
 Db 105 Q-----FMKLNVRIRNRHSCFTEBQVYSKIIVEVKPF-----QITCN--SYQTLVNST 152
 Qy 175 ITWYMGCYKIQONPNVPIPE-GMNLSPILALISNNGYTCVVTYPERGRTFHTLTLTVAY 233
 Db 153 -SLYKCKLLLENNKQPIKKAER-----EDQGYSSCVHFLHNGKLFNITKTNTIT 206
 Qy 234 VSPKNAVPVPHSPNDHYVEKEPEGELLICTVYFSLMDSRNEVMTIDGKDDIT 293
 Db 207 VEDRSNIVPVLGPKLNHVAVEL--GKNVRLNC-----SALNBEVDIYMMFGENGSDPN 260
 Qy 294 IDVTINESISHSTEDERT-----OILSIKVTSEDLKRSYVCHASAKGEVAKA 345
 Db 261 I-----HEEKEMRIMTPGKMHASKVLRLENIGESLNLVNYCTVASTGTDTKSF 311
 Qy 346 KVKOK-----VPAARYVELAGSGFATVLI---VLLIYVHYVYLMVLPYRAHGTDE 397
 Db 312 ILVRKADMDIPGHVFT-----RGMIIAVILVAVCLVTCVYRVDLVLFYRHLTERDE 367
 Qy 398 TILDGEYDIYVSAR-----NAEERFVLLTLRGVLENEFGKLCIFDRDSLPGANTVE 452
 Db 368 TLDGTYTAFVSLKECPRENEHTFAVEILPRVLEKHFGLKCFERDVVPGAAVD 427
 Qy 453 AVDFIORSRMIVLSPDYTEKSIISMLEFKL-GVMCONSIAATKLIIVYERPLHHPH-- 509
 Db 428 EIHSLIEKSRRLIIVLSKYSMSNEVYELSGIHEALVERKI--KIILIEFTVTDTFTL 485
 Qy 510 PGILOKESVSPVSKGSKSGSKGSKFKWALRLALPLRSL 549
 Db 486 POSTKLKSHRVLKWKADKSLSYNSRFWKLILYIMPAKTV 525

RESULT 10

US-09-173-151A-28
 ; Sequence 28, Application US/09173151A
 ; Patent No. 6326472
 ; GENERAL INFORMATION:
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Debets, Johannes Eduard Maria
 ; APPLICANT: Antonius
 ; APPLICANT: Sana, Theodore R.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kasteleijn, Robert A.
 ; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PC-DOS/MS-DOS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/173,151A
 ; FILING DATE: 14-OCT-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-173-151A-28

Query Match      14.4%; Score 528; DB 4; Length 541;
Best Local Similarity 30.0%; Pred. No. 8.2e-43;
Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

Db      4 LMCVSLYFYGILOSASERCDDMGDLTMR-QIOVFEDPARIK-CPLEHFLKFNSTYA 61
      10 LMWLISY-----STAESC-----TSRPHITVGEPEFLKHC-----SCSLA 46
      62 HSAGLT-LTWYTRQDDLEPINFRLPENRISKEKDVLMFRPTLNDTGNVTLMLNTT 120
      47 HEIETTKSYKSGSGSEHNE-LNPR-SSSRIALHDCVLEFWPEVLELNDTSYFFQMKNYT 104
      121 YCSKVAPELVQ--KDSFCN---SPMKLPVHKLYIEGIQRTCPNVGVFPSSVYKPT 174
      105 Q---KKKLNVIRNKGSCFTEKQVTSKIVEKKEF-----QITCEN--SYQTLVNST 152
      175 ITWYMGCYKIQNFNNVLP-GMNLSFLIALISNNGNTCVVYTPENGRTFLTRTLTKV 233
      153 -SLYKCKKLLLENNKRPYTKKNAEF-----EDGYYSCHPFLHNGKLFNITKTFNITI 206
      234 VGSFKNAVPPVHSPNDHYVEKEPGEELLIPCTVYSSFLMDSRNRYWMTIDKKPPDIT 293
      207 VEDRSNIVPVLGPKLHNAVEL--GKNVRLNC-----SALINBEDVYIMFGENGSDPN 260
      294 IDVTINESISHSRTDETRT-----QILSIKVTSEDLKRSYVCHASAKGEVAKAA 345
      261 I-----HEEKEMELMPEEGKMHASKVLRIRENIGESNLNLVYNCTVASTGTDFKSF 311
      346 KVKOK-----VPAPRYVELACGAGATYL---VYILIVYHVVWMLVLPYRAHFGIDE 397
      312 ILVKAAMADIPGHVFT---RGMILAVLIVAAVCLATVCVIRVDVILTRRDE 367
      398 TILDGKEDIVSYAR-----NAEEEFVLLTLRGVLENEGYKCTFDRDLSFGQNTVE 452
      368 TLDGKTYDAFVSYLKEGRPENGEHTFAVAILPRVLEKHYGLCTIFERIVVGGAVVD 427
      453 AVPFQIORSRMIVLSPDYVTEKISMLERFL-GVMQNSIATKLIVERYPLSEHPH-- 509
      428 EIHSLIEKSRRLIIVLSKYSYMSNEVRYELSEGLEHALVERKI--KILILEPTPVTDFTFL 485

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Db      510 PGILQKESVFSVMKGEKSKSGSKFMKALRLALPLRSIL 549
      486 PSLKLLKSHRVLKWKADKSLSYNSRPFMWOLLYLMKAKTY 525

RESULT 11
US-09-578-178-2
Sequence 2, Application US/09578178
Patent No. 6451760
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2P1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/578,178
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/110,618
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756922
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-578-178-2

Query Match      14.4%; Score 528; DB 4; Length 541;
Best Local Similarity 30.0%; Pred. No. 8.2e-43;
Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

Db      4 LMCVSLYFYGILOSASERCDDMGDLTMR-QIOVFEDPARIK-CPLEHFLKFNSTYA 61
      10 LMWLISY-----STAESC-----TSRPHITVGEPEFLKHC-----SCSLA 46
      62 HSAGLT-LTWYTRQDDLEPINFRLPENRISKEKDVLMFRPTLNDTGNVTLMLNTT 120
      47 HEIETTKSYKSGSGSEHNE-LNPR-SSSRIALHDCVLEFWPEVLELNDTSYFFQMKNYT 104
      121 YCSKVAPELVQ--KDSFCN---SPMKLPVHKLYIEGIQRTCPNVGVFPSSVYKPT 174
      105 Q---KKKLNVIRNKGSCFTEKQVTSKIVEKKEF-----QITCEN--SYQTLVNST 152
      175 ITWYMGCYKIQNFNNVLP-GMNLSFLIALISNNGNTCVVYTPENGRTFLTRTLTKV 233
      153 -SLYKCKKLLLENNKRPYTKKNAEF-----EDGYYSCHPFLHNGKLFNITKTFNITI 206
      234 VGSFKNAVPPVHSPNDHYVEKEPGEELLIPCTVYSSFLMDSRNRYWMTIDKKPPDIT 293
      207 VEDRSNIVPVLGPKLHNAVEL--GKNVRLNC-----SALINBEDVYIMFGENGSDPN 260
      294 IDVTINESISHSRTDETRT-----QILSIKVTSEDLKRSYVCHASAKGEVAKAA 345

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Db 261 I-----HEEKEMRIMTPEGKMHASKVLRILENIGESNINLVNCTVASTGTDTKSF 311
 QY 346 KVKOK-----VPAARYVELACGATVLT---VVLIVYHVMEMVLFYRAHPGTDE 397
 Db 312 ILVFKADMADIPGHVFT---RGMIIAVLIVAVCVATVYRVLVLFYRHLTRDE 367
 QY 398 TIIDGKEYDIYVSAR-----NAEEEFVLLTTRGVLENEGYKLCIFEDSDLPFGATVE 452
 Db 368 TLDGKYDAFVSLKCRRENGEHTFAVEILPRVLEKHFYGLCTFERDVYGGAVVD 427
 QY 453 AVDFIQRSRMIVLSPDVTEKSIEMLEPKL-GVMCONSIAKTLIVEXRPLEHPH- 509
 Db 428 EIHSLIKESRRLIIVLSKYSMSNEVRYELSGLHEALVERKI--KILILEFTPTDPTFL 485
 QY 510 PGLQKESVSPVSMKEKSKHSGSKFWKALRLALPLRLS 549
 486 POSLKLKSHRVLMKADKSLSYNSRPMKOLLVLMYPAKTV 525

RESULT 12

US-08-996-338-20
 ; Sequence 20, Application US/08996338
 ; Patent No. 6087116
 ; GENERAL INFORMATION:
 ; APPLICANT: TORIGOE, Kakuji
 ; APPLICANT: OKURA, Takamori
 ; APPLICANT: KURIMOTO, Masashi
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/996,338
 ; FILING DATE: 22-DEC-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 74,697/1997
 ; FILING DATE: 12-MAR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 215,488/1997
 ; FILING DATE: 28-JUL-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 291,837/1997
 ; FILING DATE: 09-OCT-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: TORIGOE-3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 521
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-996-338-20

Query Match 14.2%; Score 520; DB 3; Length 521;
 Best Local Similarity 30.5%; Pred. No. 4.7e-42;
 Matches 167; Conservative 89; Mismatches 209; Indels 82; Gaps 24;

QY 35 IOVEDEPARIK-CPLFEHFLKFNSTASAGTLT-IWWTRODRDIEEPINFLPENRI 92
 Db 9 ITVEGEPEFYLLKIC-----SCSLAHEIETTKSMYKSSGSGQEHVE-LNRP-SSSRI 57
 QY 93 SKEKDVLMREPTLANTGNATCYLKRNTYYSKAPLEVVQ--KDSGFN-----SPMLPLV 146
 Db 58 ALHDCVLEFMPVPELNDTGSFFQMKRYTQ--KMKLANVIRRNKHSCTFERQVYSKIVEV 113
 QY 147 HKLYIEYGIORICPVVDGFPSPVPTLTWYMGCKYQNFNNVPIE-GNNLSPLALIS 205
 Db 114 KKEF-----QITCEN--STYQTLVNST-SLYKCKKLLNNKNPFIKKNAEF-----E 159
 QY 206 MNGNYTCVVYTPENGRTFHLTRLTIVKVGSPKGAAPVPIHSPNDHVEKEPGEELLIP 265
 Db 160 DQGYSCVHFLHNGKLPNTTKTFNITIVEDRSNIVPVLLGPKLNHVAVEL--GQAVRLN 217
 QY 266 CTVYFSPFLMDSRNEVWTTDGGKPPDITTDVTNESISHSRTEDERT-----OILS 317
 Db 218 C---SALINEEDVVIYWMFGEENGSDPNI-----HEEKEMRIMTPEGKMHASKVLR 264
 QY 318 IKKVTSEDLKRSYVCHASAKGEVAKAKVKOK-----VPAARYVELACGATVLT--- 370
 Db 265 IENIGESNLMVLTCTVASTGTDTKSFILVRKOMADIPGHVFT---RGMIIAVLIVA 320
 QY 371 VVLIVYHVMEMVLFYRAHFGTDETIIDGKEYDIYVSAR-----NAEEEFVLLTL 425
 Db 321 VGLVAVCVIYRVDVLFYRHLTRDETLTGTYDAFVSLKCRRENGEHTFAVEIL 380
 QY 426 RGVLENEGYKLCIFEDSDLPFGATVEAVDFIQRSRMIVLSPDVTEKSIEMLEPKL 485
 Db 381 PRVLEKHFYGLCTFERDVYGGAVVDEIHSLEKSRRLIIVLSKYSMSNEVRYELSGL 440
 QY 486 -GVMCONSIAKTLIVEXRPLEHPH--PGLQKESVSPVSMKEKSKHSGSKFWKALRL 542
 Db 441 HEALVERKI--KILILEFTPTDPTFLPSLKLKSHRVLMKADKSLSYNSRPMKOLLV 498
 QY 543 ALPLRLS 549
 Db 499 LMPAKTV 505

RESULT 13

US-09-173-151A-32
 ; Sequence 32, Application US/09173151A
 ; Patent No. 6326472
 ; GENERAL INFORMATION:
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Debets, Johannes Eduard Maria
 ; APPLICANT: Antonius
 ; APPLICANT: Sana, Theodore R.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kastelein, Robert A.
 ; TITLE OF INVENTION: Human Receptor Proteins, Related Reagents and Methods
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/173,151A
 ; FILING DATE: 14-OCT-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/065,776
 ; FILING DATE: 17-NOV-1997

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      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 60/078,008
      FILING DATE: 12-MAR-1998
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 60/081,883
      FILING DATE: 15-APR-1998
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 60/095,987
      FILING DATE: 10-AUG-1998
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 60/078,416
      FILING DATE: 18-MAR-1998
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 60/062,066
      FILING DATE: 15-OCT-1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Ching, Edwin P.
      REGISTRATION NUMBER: 34,090
      REFERENCE//DOCKET NUMBER: DX0767X
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (650)852-9196
      TELEFAX: (650)496-1200
      INFORMATION FOR SEQ ID NO: 32:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 555 amino acids
      TYPE: amino acid
      STRANDEDNESS: not relevant
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      US-09-173-151A-32

Query Match      13.5%; Score 496; DB 4; Length 555;
Best Local Similarity 26.4%; Pred. No. 1.2e-39;
Matches 155; Conservative 109; Mismatches 230; Indels 94; Gaps 26;

      6 CVALYFYGILQSDASERCDMDGLTMKQIQVFEDEPARIKCPLEHFLKFNYSSTAHSAG 65
      26 CVICNRY-----VINGEPALISCPV-----ITLPMLS-D 54

      66 LTLIWTTRQDRDLDEEPINFLPENRISKEKQVLMFRPTLLINDTGNVTOMLNTTYSKV 125
      55 YNLTWY--RINGSNM--PITTE-RRARIHQKQLMFTIPALAEISGLYCEVRSILRSKQK 109

      126 APLLEVQKDS--CENSFMKLPVHKLYIEGIQRTICPNVGY--PRSSVKPTITMYMCKY 182
      110 IINKVFQNDGICFNGEMK--YDQIVKSANAGKICPDLNFKQEDININBIHMYECK 167

      183 K--IQFNNAVIPGMN--LSPILALISNNGNTVCVVTYPENGRFTLTLTKVVSFKN 239
      168 SGFLDKRLVLABGNALILINVTIQDKGNTCIRNVITYMKQYVSTNMLEVYESLTK 227

      240 AVPVVHSPNDVHYEKEGSEELLIPCTV---YESFLMDSRNEVWMTIDKKPDITIV 296
      228 MRPEFIY--PNNNTI-EVGLSGHVHVECVSSGVGLL-----PYMQVNDSDVD--SPDS 277

      297 T-----INESISHRTBETRTQILSIKQVTSBDLKRSYVCARAKAEVAKAKVKQKV 351
      278 TYRQOFTEEGMPHGIANSGR--FNISEVKIKDYAKYFPGHFIYDSQEFSTYIKLH-- 332

      352 PAPRYVELACGATVLLVLLVYVHYVLMELVLYRA--HFGTDEITLDGEYDIYV 409
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      410 SYARNAR-----EEEFVLLTRGVLEENEGYKLCIFDRDSLPGAGTVAEVPFIORSRM 464
      393 LYPKRESCLVSDIFALKILPEVLEEROCGVNLFIFGNNDLAGEVIVDTEKIHQSHRV 452

      465 IVLVSP-----DYVTEKISIMLEFLGWGCONSIATKLIIVGYRPL--HHPHIL 513
      453 IILVPESCGILEDASEKHLAV---YNALIDGCI--KILILELEKIEDYANNPESIK 506

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RESULT 14
US-07-821-716-4
Sequence 4, Application US/07821716
Patent No. 5319071
GENERAL INFORMATION:
APPLICANT: Dower, Steven K.
APPLICANT: March, Carl J.
APPLICANT: Sims, John
APPLICANT: Urdal, David L.
TITLE OF INVENTION: Soluble Interleukin-1 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/821,716
FILING DATE: 19920114
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 125627
FILING DATE: 25-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160550
FILING DATE: 25-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 258756
FILING DATE: 13-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691551
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE//DOCKET NUMBER: 2001-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
FAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-821-716-4

Query Match      13.2%; Score 484.5; DB 1; Length 576;
Best Local Similarity 25.8%; Pred. No. 1.7e-38;
Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;

      34 QIQVFEDEPARI-----KCPLEHFLKFNYSSTAHSAGTLIWTTRQDRDLDEE 81
      21 EIDVCTEYPQIVLFSVNEIDIRKCPLEPNKWH-----GDTIHW-----KNDSKT 67

      82 PINFRLDENRISKEKQVLMFRPTLLINDTGNVTQMLNNTTYSKVAFLLEVQKDS--CFN 139
      68 PISAD-RDSRIHQNEHLMWVPAKVDSGYTCIVRNSITCLTKKYVTVLENDPGLCTYS 126

      140 SPKLPVHKLYIEGIQRTICPNVGYF--PSSVKPTITMYMCKYKIQNINNAVIPSGMNL 197
      127 TOATFP-QRLHIA-GDSGLVCPYV-SYFKDENNELPEVQWYKNC-KPLLDNVSFFGVKD 182

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QY 198 SPILALIS--NNGNYTCVTPYENGRTFHLTRILTVKVGSPKXNAVPPVHSPNDHYVE 255
 DB 183 KLLVRVAEHRDGYICRMSYFRGQYPTRVIOFITIDENKRD-RPVILSPRNETI-E 240
 QY 256 KEGEELLICCTYFSTFLMSRNEVMTIDGKPDITITVINES-----ISHSRT 307
 DB 241 ADGSMIQLCNVTGQF-----SDLVYMKNGS-----EIEWDPFLADYOFVEHPST 289
 QY 308 EDE-TRTOILSIKKVTSBIDLKRSYVCHASAKGEVAKAKVOKVAPRYVELACFGA 366
 DB 290 KRKYTLITTLNISSEVKSQFRYPFICVVKNT--NIFSAHVOLIVPDPKNTLIGFII 347
 QY 367 TVLLVYILIVVHYVLEWVLFYRAHFG--TDETLIDGKEYDIYVSYARNAE-----E 418
 DB 348 LRTATVCCVCICYKVFVDIYLMWRDSCSGFLPSKASDGKTYDAYILYPTLGEFSFSDLD 407
 QY 419 EFWLLTRGVLENEFGYKLCIFDRDSLPGCNTVEAFDFIORSRMTIVLSPD-----471
 DB 408 TVFVKLLPEVLEGGQFYKLFYGRDDYVGEDTIEVTNENVKSRLLIILVRDMGFSWL 467
 QY 472 -YTEKSISMLBFLGVMCONSIA TKLIVBYRPLE--HPHGILO-LKESVFSVMKG- 526
 DB 468 GGSSEBQIAL---YNALIOEGI--KIVLELEKIQDYERMPDSIQFKQKGVICWSD 521
 QY 527 --EKSXHSKSKFWKALRLALPLRSLSASGWNESCSQSDISLDHYQRRSRRL 577
 DB 522 FQBRPQSAKTRFWKMLRYQMPAQRSS-----PLSKHRLTLIDPVDRYTERKL 567

RESULT 15

US-08-381-603-4
 ; Sequence 4, Application US/08381603
 ; Patent No. 5858355

GENERAL INFORMATION:

APPLICANT: Glorioso, Joseph C.
 APPLICANT: Evans, Christopher H.
 TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue of a
 TITLE OF INVENTION: Mammalian Host
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eckert Seamans Cherin & Mellott
 STREET: 1700 Market Street Suite 3232
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/381,603
 FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Gould, Jr., Lewis P.
 REGISTRATION NUMBER: 25,057
 REFERENCE/DOCKET NUMBER: 109070-11
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 575-6000
 TELEFAX: (215) 575-6015
 TELEX: 866172

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 576 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-381-603-4

Query Match

13.2%; Score 484.5; DB 2; Length 576;

Best Local Similarity 25.8%; Pred. No. 1.7e-38;
 Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;
 QY 34 QIOVFEDPARI-----KCPLEHFLKFNYSIAHAGLTLIYMTWRQDDLE 81
 DB 21 EIDVCTEYNQIVLFLSVNEIDRCPKLPNKKH-----GDTIYV---KNDSKT 67
 QY 82 PINFRLEPNRISKEKOVLFNFRPLTNDTGNNTYCMLENTYCSKVAPPELVQKDS--CFN 139
 DB 68 PISAD-RDSRIHQONHLMFVPAKVEDSGYICYANSTYCLTKTYVLENDPGLCTS 126
 QY 140 SPMKLPVHKLYIEYGIQRTCPNVGDYF--PSSVKPTITWGCYKIQNFNNVPIPGMUL 197
 DB 127 TQATFP-ORLHIA-GGSLVCEPV--SYFRDNNELPEVQMYKNC-KPLLDVVSFFGVGD 182
 QY 198 SPILALIS--NNGNYTCVTPYENGRTFHLTRILTVKVGSPKXNAVPPVHSPNDHYVE 255
 DB 183 KLLVRVAEHRDGYICRMSYFRGQYPTRVIOFITIDENKRD-RPVILSPRNETI-E 240
 QY 256 KEGEELLICCTYFSTFLMSRNEVMTIDGKPDITITVINES-----ISHSRT 307
 DB 241 ADGSMIQLCNVTGQF-----SDLVYMKNGS-----EIEWDPFLADYOFVEHPST 289
 QY 308 EDE-TRTOILSIKKVTSBIDLKRSYVCHASAKGEVAKAKVOKVAPRYVELACFGA 366
 DB 290 KRKYTLITTLNISSEVKSQFRYPFICVVKNT--NIFSAHVOLIVPDPKNTLIGFII 347
 QY 367 TVLLVYILIVVHYVLEWVLFYRAHFG--TDETLIDGKEYDIYVSYARNAE-----E 418
 DB 348 LRTATVCCVCICYKVFVDIYLMWRDSCSGFLPSKASDGKTYDAYILYPTLGEFSFSDLD 407
 QY 419 EFWLLTRGVLENEFGYKLCIFDRDSLPGCNTVEAFDFIORSRMTIVLSPD-----471
 DB 408 TVFVKLLPEVLEGGQFYKLFYGRDDYVGEDTIEVTNENVKSRLLIILVRDMGFSWL 467
 QY 472 -YTEKSISMLBFLGVMCONSIA TKLIVBYRPLE--HPHGILO-LKESVFSVMKG- 526
 DB 468 GGSSEBQIAL---YNALIOEGI--KIVLELEKIQDYERMPDSIQFKQKGVICWSD 521
 QY 527 --EKSXHSKSKFWKALRLALPLRSLSASGWNESCSQSDISLDHYQRRSRRL 577
 DB 522 FQBRPQSAKTRFWKMLRYQMPAQRSS-----PLSKHRLTLIDPVDRYTERKL 567

Search completed: April 23, 2003, 08:55:30
 Job time : 34 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:54:06 ; Search time 45 Seconds

(without alignments)
1223.315 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVSLVYFYLQSDA.....SALALHFTDLSNNDFYLL 687

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2586	70.5	570	9	US-10-011-548-36	Sequence 36, Appl
2	2580	70.3	570	9	US-10-215-211-4	Sequence 4, Appl
3	2327.5	63.4	570	9	US-10-011-548-21	Sequence 21, Appl
4	1934	52.7	359	9	US-10-215-211-6	Sequence 6, Appl
5	1930	52.6	910	9	US-09-935-868-28	Sequence 28, Appl
6	825	22.5	686	9	US-10-011-548-4	Sequence 4, Appl
7	800	21.8	579	9	US-10-011-548-2	Sequence 2, Appl
8	762.5	20.8	668	9	US-10-011-548-35	Sequence 35, Appl
9	528	14.4	541	9	US-10-011-548-28	Sequence 28, Appl
10	528	14.4	541	10	US-09-981-421-4	Sequence 4, Appl
11	528	14.4	541	12	US-10-157-447-2	Sequence 2, Appl
12	496	13.5	555	9	US-10-011-548-32	Sequence 32, Appl
13	484.5	13.2	576	9	US-10-011-548-30	Sequence 30, Appl
14	484.5	13.2	576	10	US-09-731-175-4	Sequence 4, Appl
15	479	13.1	537	9	US-10-011-548-29	Sequence 29, Appl
16	479	13.1	537	12	US-10-157-447-4	Sequence 4, Appl
17	478	13.0	567	9	US-10-011-548-24	Sequence 24, Appl
18	478	13.0	567	9	US-10-004-633-39	Sequence 39, Appl
19	478	13.0	567	10	US-09-899-980A-7	Sequence 7, Appl

20	471.5	12.9	599	9	US-09-731-449-2	Sequence 2, Appl
21	471.5	12.9	599	9	US-10-212-287-7	Sequence 7, Appl
22	471.5	12.9	599	9	US-10-011-548-10	Sequence 10, Appl
23	471.5	12.9	599	10	US-09-981-421-2	Sequence 2, Appl
24	471	12.8	580	9	US-09-731-449-8	Sequence 8, Appl
25	463.5	12.6	556	10	US-09-899-980A-8	Sequence 8, Appl
26	457	12.5	561	9	US-10-011-548-23	Sequence 23, Appl
27	457	12.5	561	10	US-09-775-046-15	Sequence 15, Appl
28	446	12.2	614	9	US-10-212-287-2	Sequence 2, Appl
29	446	12.2	614	9	US-10-011-548-16	Sequence 16, Appl
30	445	12.1	610	9	US-10-011-548-14	Sequence 14, Appl
31	444.5	12.1	562	9	US-10-011-548-22	Sequence 22, Appl
32	444.5	12.1	562	10	US-09-775-046-13	Sequence 13, Appl
33	436	11.9	467	9	US-10-011-548-8	Sequence 8, Appl
34	424.5	11.6	569	9	US-10-011-548-31	Sequence 31, Appl
35	424.5	11.6	569	10	US-09-840-707A-3	Sequence 3, Appl
36	424.5	11.6	569	10	US-09-731-175-2	Sequence 3, Appl
37	414	11.3	486	9	US-10-011-548-20	Sequence 20, Appl
38	413.5	11.3	481	10	US-09-764-853-655	Sequence 655, App
39	392	10.7	70	10	US-09-864-761-48704	Sequence 48704, A
40	314	8.6	410	9	US-10-011-548-27	Sequence 27, Appl
41	314	8.6	410	9	US-10-199-209-13	Sequence 13, Appl
42	290.5	7.9	217	9	US-09-731-449-11	Sequence 11, Appl
43	252	6.9	398	9	US-10-215-211-2	Sequence 2, Appl
44	252	6.9	398	9	US-10-011-548-26	Sequence 26, Appl
45	252	6.9	398	9	US-10-199-209-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-011-548-36
; Sequence 36, Application US/10011548
; Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Antoniuss
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
METHODS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-Nov-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-Mar-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-Apr-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-Aug-1998
APPLICATION NUMBER: US 60/078,416

FILE REFERENCE: 3321-A
CURRENT APPLICATION NUMBER: US/10/215,211
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/310,789
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 570
TYPE: PRT
ORGANISM: Homo sapiens
US-10-215-211-4

Query Match
Best Local Similarity 70.5%; Score 2586; DB 9; Length 570;
Matches 487; Conservative 31; Mismatches 45; Indels 6; Gaps 3;

1 MTLIMCVSLIFYGIIQSDASERCDMDGLDMRQIQVFEDPARIKCPLEHFLKPNYST 60
1 MTLIMCVSLIFYGIIQSDASERCDMDGLDMRQIQVFEDPARIKCPLEHFLKPNYST 60
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121 YCSKVAPELVQKDSGFNSPMKLPVHKLIEYGIQRTCPNDGVPSSVKPPTITMYMG 180
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LEFLGVGMCONSITAT---LIYVERPLLEHPHPIQLKES---VSFVSKGEKSKHSG 533
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SKFWKALRLALPLRSLASAGNESCOSQSDI 565
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RESULT 2
US-10-215-211-4
Sequence 4, Application US/10215211
Publication No. US20030049255A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Smith, Dirk E.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES

FILE REFERENCE: 3321-A
CURRENT APPLICATION NUMBER: US/10/215,211
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/310,789
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 570
TYPE: PRT
ORGANISM: Homo sapiens
US-10-215-211-4

Query Match
Best Local Similarity 70.3%; Score 2580; DB 9; Length 570;
Matches 487; Conservative 31; Mismatches 45; Indels 6; Gaps 3;

1 MTLIMCVSLIFYGIIQSDASERCDMDGLDMRQIQVFEDPARIKCPLEHFLKPNYST 60
1 MTLIMCVSLIFYGIIQSDASERCDMDGLDMRQIQVFEDPARIKCPLEHFLKPNYST 60
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LEFLGVGMCONSITAT---LIYVERPLLEHPHPIQLKES---VSFVSKGEKSKHSG 536
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481 LEFLGVGMCONSITAT---LIYVERPLLEHPHPIQLKES---VSFVSKGEKSKHSG 536
481 LEFLGVGMCONSITAT---LIYVERPLLEHPHPIQLKES---VSFVSKGEKSKHSG 536
WKAALRLALPLRSLASAGNESCOSQSDI 565
WKAALRLALPLRSLASAGNESCOSQSDI 565
539 WKQLOVAMPVAKSPRRSSSDDEGLSYSSL 567
539 WKQLOVAMPVAKSPRRSSSDDEGLSYSSL 567

RESULT 3
US-10-011-548-21
Sequence 21, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Debets, Johannes Eduard Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

```

Db 301 SVSVSSTDETRTQILSIKKYTPEDLRBNVYCHANTNGEAGQAAKVOKVPIPRYTEL 360
Qy 361 ACGGATYLLVVLIVVTHVYVWLENVLFYRAHFGTDEITLDOGKEVDIYVSARNAEEBF 420
Db 361 ACGGATYELVVVLLVYVHVYVWLENVLFYRAHFGTDEITLDOGKEVDIYVSARNAEEBF 420
Qy 421 VLLTLRGLENEPGKLCIFDRDSLPGENTVAEVPFIORSRBMVLSPPDVTEKSISM 480
Db 421 VLLTLRGLENEPGKLCIFDRDSLPGGIYVDETLSFIOKSRLLVLVSPNVLOGTQAL 480
Qy 481 LEFKLGVACONSIAVK---LIVEYRPLEHPHPGILQIKES---VSFVSWGKSKSHG 533
Db 481 LELKAGL---ENMASRGNINILVQYKAVKQMK--VKELKRAKVTVLTVIKWGEKSKYRQ 535
Qy 534 SKFWALRLLALPLNSLSASSGWNES 558
Db 536 GRFWKOLQVAMPVKK---SPRWSSN 557

RESULT 4
US-10-215-211-6
; Sequence 6, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215, 211
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310, 789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-211-6

Query Match 52.7%; Score 1934; DB 9; Length 359;
Best Local Similarity 99.7%; Pred. No. 7,66-148;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1 MTLIMCVSLYFYGILOSASERCDDWGLDTMRQIQVEFDEPARIKCPLFEHFLKFNYS 60
Db 1 MTLIMCVSLYFYGILOSASERCDDWGLDTMRQIQVEFDEPARIKCPLFEHFLKFNYS 60
Qy 61 AHSAGLTITVWTRDRLPEEPINRLPEBNRISKQDVLMPRPITLANTGNTCMLRNT 120
Db 61 AHSAGLTITVWTRDRLPEEPINRLPEBNRISKQDVLMPRPITLANTGNTCMLRNT 120
Qy 121 YCSKAPLELVVQKSCNSPKMLPVHGLYIEYGIQRTCPVNDGYFPSSVAPRTITWNG 180
Db 121 YCSKAPLELVVQKSCNSPKMLPVHGLYIEYGIQRTCPVNDGYFPSSVAPRTITWNG 180
Qy 181 CYKIQNFNNVPIPEGNNISFLIALISNNNGYTCVVYTPENGRTFHLTRLTVRVGSPKXA 240
Db 181 CYKIQNFNNVPIPEGNNISFLIALISNNNGYTCVVYTPENGRTFHLTRLTVRVGSPKXA 240
Qy 241 VPPVTHSHNDHVYIEKEGEBELLICTYVYFSLMDSRNBWMTIDGKKPDDITDVTINE 300
Db 241 VPPVTHSHNDHVYIEKEGEBELLICTYVYFSLMDSRNBWMTIDGKKPDDITDVTINE 300
Qy 301 SISHSRTDETRTQILSIKKYTSBDLKSYCHASAGVAKAKVOKVAPRYTVE 359
Db 301 SISHSRTDETRTQILSIKKYTSBDLKSYCHASAGVAKAKVOKVAPRYTVE 359

```

GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENGTH: 910
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-868-28

Query Match 52.6%; Score 1930; DB 9; Length 910;
Best Local Similarity 99.7%; Pred. No. 6,3e-147;
Matches 357; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLKCVSLIYFYGILOSASERCDMDGLTMRQIQVPEDEPARIKCPLEHFLKENVST 60
1 MVLKCVSLIYFYGILOSASERCDMDGLTMRQIQVPEDEPARIKCPLEHFLKENVST 60
DB 61 AHSAGLTLIWMYTRDRLDEPINFRLPENRISKEKDVLMFRPLTLDGTGNTMLNNTT 120
61 AHSAGLTLIWMYTRDRLDEPINFRLPENRISKEKDVLMFRPLTLDGTGNTMLNNTT 120
QY 121 YCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVGYPSSVKPTITWYMG 180
121 YCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVGYPSSVKPTITWYMG 180
DB 121 YCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVGYPSSVKPTITWYMG 180
121 YCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVGYPSSVKPTITWYMG 180
QY 181 CYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTRLTVKVGSPNA 240
181 CYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTRLTVKVGSPNA 240
DB 181 CYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTRLTVKVGSPNA 240
181 CYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTRLTVKVGSPNA 240
QY 241 VPPVHSPNDHVYKEKRGEBLLPCTVYFSLMDSRNEVWTTIDGKKPDITIDVTINE 300
241 VPPVHSPNDHVYKEKRGEBLLPCTVYFSLMDSRNEVWTTIDGKKPDITIDVTINE 300
DB 241 VPPVHSPNDHVYKEKRGEBLLPCTVYFSLMDSRNEVWTTIDGKKPDITIDVTINE 300
241 VPPVHSPNDHVYKEKRGEBLLPCTVYFSLMDSRNEVWTTIDGKKPDITIDVTINE 300
QY 301 SISHSRTEDTRQILSIKVTSEDLKRSYVCHARSAGVAKAVAKVQKVPARITY 358
301 SISHSRTEDTRQILSIKVTSEDLKRSYVCHARSAGVAKAVAKVQKVPARITY 358
DB 301 SISHSRTEDTRQILSIKVTSEDLKRSYVCHARSAGVAKAVAKVQKVPARITY 358
301 SISHSRTEDTRQILSIKVTSEDLKRSYVCHARSAGVAKAVAKVQKVPARITY 358

RESULT 6
US-10-011-548-4
Sequence 4, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Debets, Johannes Eduard Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kastelen, Robert A.
TITLE OF INVENTION: Human Receptor Proteins, Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548

FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-Nov-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-Mar-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-Apr-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-Aug-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-Mar-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 686 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-011-548-4

Query Match 22.5%; Score 825; DB 9; Length 686;
Best Local Similarity 31.9%; Pred. No. 4,9e-58;
Matches 228; Conservative 106; Mismatches 244; Indels 136; Gaps 27;

QY 1 MTLKCVSLIYFYGILOSASERCDMDGLTMRQIQVPEDEPARIKCPLEHFLKENVST 59
1 MTLKCVSLIYFYGILOSASERCDMDGLTMRQIQVPEDEPARIKCPLEHFLKENVST 59
DB 7 LALVCSVSTNLKMWKRSVDCIDWSVD-LKTYMALAGEVRYKCALFYSTIRTNYS 65
7 LALVCSVSTNLKMWKRSVDCIDWSVD-LKTYMALAGEVRYKCALFYSTIRTNYS 65
QY 60 TASHAGLTLIWMYTRDRLDEPINFRLPENRISKEKDVLMFRPLTLDGTGNTMLNNTT 119
60 TASHAGLTLIWMYTRDRLDEPINFRLPENRISKEKDVLMFRPLTLDGTGNTMLNNTT 119
DB 66 TASHAGLTLIWMYTRDRLDEPINFRLPENRISKEKDVLMFRPLTLDGTGNTMLNNTT 119
66 TASHAGLTLIWMYTRDRLDEPINFRLPENRISKEKDVLMFRPLTLDGTGNTMLNNTT 119
QY 120 TYCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVGYPSSVKP 173
120 TYCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVGYPSSVKP 173
DB 122 TYCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVGYPSSVKP 173
122 TYCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVGYPSSVKP 173
QY 174 TITWYMGCTYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTRLTVK 233
174 TITWYMGCTYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTRLTVK 233
DB 176 DVVWYKECKRQWRSIIIOGNALLIOEVOEEDGANTYCEKLT--EKKL--VRRTELKV 231
176 DVVWYKECKRQWRSIIIOGNALLIOEVOEEDGANTYCEKLT--EKKL--VRRTELKV 231
QY 234 VGSPPKAVP-PVHSPNDHVYKEKRGEBLLPCTVYFSLMDSRNEVWTTIDGKKPDIT 292
234 VGSPPKAVP-PVHSPNDHVYKEKRGEBLLPCTVYFSLMDSRNEVWTTIDGKKPDIT 292
DB 232 TALLTDKPPKPLFPMENQPSVIDVQKPLNTFCFAFGSGSGSPITV--MAGEK---- 286
232 TALLTDKPPKPLFPMENQPSVIDVQKPLNTFCFAFGSGSGSPITV--MAGEK---- 286
QY 293 TIDVTINESISHSRTEDTR-----TQILSIKVTSEDLKRSYVCHARSAGV 341
293 TIDVTINESISHSRTEDTR-----TQILSIKVTSEDLKRSYVCHARSAGV 341
DB 287 -----FIELAGHIR-BGEIRLKEHLEKEVEELALIPDSVEADL--ANYCHVENRNGR- 339
287 -----FIELAGHIR-BGEIRLKEHLEKEVEELALIPDSVEADL--ANYCHVENRNGR- 339
QY 342 AKAAKVVQKVPARITYVELACGATVLLVIVVHVVMVLFYRAHFGDETIID 401
342 AKAAKVVQKVPARITYVELACGATVLLVIVVHVVMVLFYRAHFGDETIID 401
DB 340 -KASVILARKKDLIYKIELAGGALFLLVLLVVIYKCNIEMLFYRQHPGADRND 398
340 -KASVILARKKDLIYKIELAGGALFLLVLLVVIYKCNIEMLFYRQHPGADRND 398
QY 402 GKEVDIVSYAR-----NAEEEFVLLTLRGVLENEFGYKLCIFDSDSLPGGNTVE 452
402 GKEVDIVSYAR-----NAEEEFVLLTLRGVLENEFGYKLCIFDSDSLPGGNTVE 452
DB 399 NKEVDALSTTKVDQDPLDCDNPEEBEPALFVLPVLEKHYGKLPFEBDLIPSGTYME 458
399 NKEVDALSTTKVDQDPLDCDNPEEBEPALFVLPVLEKHYGKLPFEBDLIPSGTYME 458
QY 453 AVPDFIORSRMIVLSPDVYTKSISMLEFKLGVMCONSIAI--KLIVKVRPLEPH 509
453 AVPDFIORSRMIVLSPDVYTKSISMLEFKLGVMCONSIAI--KLIVKVRPLEPH 509
DB 459 DLTRYVQSRRLIIVLPDYLIRGWSI--FELESRLHNLVSGEIKVILIBCTELK--- 513
459 DLTRYVQSRRLIIVLPDYLIRGWSI--FELESRLHNLVSGEIKVILIBCTELK--- 513

SEQUENCE DESCRIPTION: SEQ ID NO: 28;
US-10-011-548-28

Query Match 14.4%; Score 528; DB 9; Length 541;
Best Local Similarity 30.0%; Pred. No. 3e-34;

Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

```

QY 4 LMCVSLYFYGIQSDASERCDDWGLDTR-QIOVFEDPARIK-CPLEHFLKFNYSTA 61
DB 10 LMLVLSV-----STAESC-----TSRPHITVEGEFPYLKHC-----SCSLA 46
QY 62 HSGAGLT-ITWTRQDRLDEPINFRLPERNISKEDVLMFRPLTNDGNTYCLMNTT 120
DB 47 HEIETTKSWYKSGSGOEHE-IMP-SSSRIALHDCVLEFWEVLELNDGSGYFFOMKNYT 104
QY 121 YGKVAAPLEVO--KDSCFN---SPMKLPVHKLTYEIGRIOTCPVNDGYPPSSVKPT 174
DB 105 Q-----KKKLVIRRNKSCFTEKROVTSKIVEKFP-----QITCEN--SYOTLVNST 152
QY 175 ITWYMGCYKIQNFNNVPIE-GMNLSPILALISNNGYTCVVTYBENGRTFHLTRTLTKV 233
DB 153 -SLYKCKKLLLENNKPTIKNAEF-----EDGYTSCVHFLHNGKLFNITKTENITI 206
QY 234 VSGPKNAVPPVHSFNDHVTYEKEPGBELLIPCTVYFSFLMDSRNEVWMTIDGKPPDIT 293
DB 207 VEDRSNIVPVLGPKNHVAVEL--GKNVRLNC---SALINEEDVLYMMFGEENGSDPN 260
QY 294 IDVTINESISHRTEDERT-----QILSIKVTSEDLKRSYVCHARSAGEVAKAA 345
DB 261 I-----HEEKEMRIPTBEGKMHASKVLRLENIGESNLAVLYNCTVASTGDTKSF 311
QY 346 KVKOK-----VPAARYVELACGFATVLL--VILLIVVHYVWLEMLFYRAHFGTDE 397
DB 312 ILVRKADMADIPGHVFT---RGMIIAVLIVAVVCLVTVYRVDLVFYRHLTRDE 367
QY 398 TILDKERYDIYVSAR-----NAEEEPVLLTLRGVLENEFGYKLCIFDRDSLPGNTVE 452
DB 368 TLTGKTYDAFVSYLKECRPENGEBHTFAVEILPRVLEKHFYKLCIFERDVVPGAAVD 427
QY 453 AVDFIORSRMTVLSPOVTEKSIEMLEFKL-GWMCNSIATKLIYVVRPLEHH-- 509
DB 428 EHSLEKSRRLIIVLSKSYNSNEVRYELSGHLEALVERKI--KILILEFTVDTFTL 485
QY 510 PGILQLESVSVSWKGEKSHSGKFKMALRLALPLRSL 549
DB 486 POSLKLKSHRVLKMADKSLSYNSRFWKLLYLMRAKTV 525

```

RESULT 10

US-09-981-421-4
Sequence 4, Application US/09981421
Patent No. US20020098185A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Mohler, Kendall M.
APPLICANT: Born, Teresa L.
TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
FILE REFERENCE: 3086-A
CURRENT APPLICATION NUMBER: US/09/981,421
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 541
TYPE: PRT
ORGANISM: Homo sapiens
US-09-981-421-4

Query Match 14.4%; Score 528; DB 10; Length 541;
Best Local Similarity 30.0%; Pred. No. 3e-34;
Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

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QY 4 LMCVSLYFYGIQSDASERCDDWGLDTR-QIOVFEDPARIK-CPLEHFLKFNYSTA 61
DB 10 LMLVLSV-----STAESC-----TSRPHITVEGEFPYLKHC-----SCSLA 46
QY 62 HSGAGLT-ITWTRQDRLDEPINFRLPERNISKEDVLMFRPLTNDGNTYCLMNTT 120
DB 47 HEIETTKSWYKSGSGOEHE-IMP-SSSRIALHDCVLEFWEVLELNDGSGYFFOMKNYT 104
QY 121 YGKVAAPLEVO--KDSCFN---SPMKLPVHKLTYEIGRIOTCPVNDGYPPSSVKPT 174
DB 105 Q-----KKKLVIRRNKSCFTEKROVTSKIVEKFP-----QITCEN--SYOTLVNST 152
QY 175 ITWYMGCYKIQNFNNVPIE-GMNLSPILALISNNGYTCVVTYBENGRTFHLTRTLTKV 233
DB 153 -SLYKCKKLLLENNKPTIKNAEF-----EDGYTSCVHFLHNGKLFNITKTENITI 206
QY 234 VSGPKNAVPPVHSFNDHVTYEKEPGBELLIPCTVYFSFLMDSRNEVWMTIDGKPPDIT 293
DB 207 VEDRSNIVPVLGPKNHVAVEL--GKNVRLNC---SALINEEDVLYMMFGEENGSDPN 260
QY 294 IDVTINESISHRTEDERT-----QILSIKVTSEDLKRSYVCHARSAGEVAKAA 345
DB 261 I-----HEEKEMRIPTBEGKMHASKVLRLENIGESNLAVLYNCTVASTGDTKSF 311
QY 346 KVKOK-----VPAARYVELACGFATVLL--VILLIVVHYVWLEMLFYRAHFGTDE 397
DB 312 ILVRKADMADIPGHVFT---RGMIIAVLIVAVVCLVTVYRVDLVFYRHLTRDE 367
QY 398 TILDKERYDIYVSAR-----NAEEEPVLLTLRGVLENEFGYKLCIFDRDSLPGNTVE 452
DB 368 TLTGKTYDAFVSYLKECRPENGEBHTFAVEILPRVLEKHFYKLCIFERDVVPGAAVD 427
QY 453 AVDFIORSRMTVLSPOVTEKSIEMLEFKL-GWMCNSIATKLIYVVRPLEHH-- 509
DB 428 EHSLEKSRRLIIVLSKSYNSNEVRYELSGHLEALVERKI--KILILEFTVDTFTL 485
QY 510 PGILQLESVSVSWKGEKSHSGKFKMALRLALPLRSL 549
DB 486 POSLKLKSHRVLKMADKSLSYNSRFWKLLYLMRAKTV 525

```

RESULT 11

US-10-157-447-2
Sequence 2, Application US/10157447
Patent No. US20020143155A1
GENERAL INFORMATION:
APPLICANT: Parinet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,447
FILING DATE: 28-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/576,178
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/110,618
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172.
 REFERENCE/DOCKET NUMBER: 2619
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 541 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-157-447-2

Query Match 14.4%; Score 528; DB 12; Length 541;
 Best Local Similarity 30.0%; Pred. No. 3e-34;
 Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

QY 4 LMCVSLYFYGLQSDASERCDMDGLDTR-QIOVFEDEPARIK-CPLFEHLKFNSTASTA 61
 DB 10 LMTLISV-----STRASC-----TSRPHITVEGEPEPTLKAC-----SCSLA 46
 62 HSAGLTL-IMWTRDRLDEEPINFLPENRISKEKDVLMFRPTLLNDTGNVTCMLRNTT 120
 DB 47 HEIETTSKWSKSSGSGEHE-IMNR-SSSRILALHDVLEFMPVELNDTGSYFQMKMYT 104
 QY 121 YCSKAPLELVQ-KDSCFN-----SPMKLPVHKLYITRGQRTCPNVDDGYFBSVQPT 174
 DB 105 Q-----KMTLANYIRNKHSCFERQVTSKIVEYKCF-----QITCEN--SYQTLVNST 152
 QY 175 ITWYWGCKIQNFNNVIE-GMNLFLIALISNNGNYTCVVTYPENGRTPHLTRLITVYKV 233
 DB 153 -SLYNCKKLLLENNKAPTIKNAEF-----EDQSYSCVHPLHNGKLFNITKTENITTI 206
 QY 234 VCSKPAVPPVILHSPNDVVEKEPEBELLPCTVYFSLMDSRNEVMTIDGKKPDIT 293
 DB 207 VEDRNIVPVLLGPKLNHVAEL-GKAVRLNC-----SALNBEVIVYMGGEENSGSPN 260
 QY 294 IDVTINESISHRTDEFTT-----QIISIKKVTSEDLKRSYVCAKSAKEVAFAA 345
 DB 261 I-----HEKEMRIIMTEGKMHASKVRIENIGESNLAVLNCVASTGTGDTGTSF 311
 QY 346 KYKOK-----VAPRYVTELACGFATVIL--VVILIVVHVWLWLVLPFRAHFGTDE 397
 DB 312 ILVRKADADIFGHVFT---RGMIIAVLILVAVCLVTVKVDLVPFRHLTRDE 367
 QY 398 TILDKEXYDIYVSAR-----NAEEEFVLLTLRGVLENERGYKLCIFDRDSLPGAGTVE 452
 DB 368 TLTDKTDAPFVSLKECKRPEGEHETFAVELPRVLEKHGYKLCIFERDVPAGAVVD 427
 453 AVFDPIQSRRIIVLSPDYTEKSIKMLEFGL-GVMCONSITATLYIVETRPLEHPI-- 509
 DB 428 EIHSLIEKSRRLIIVLSYSYMSNEVRTELESGLHVALVERKI--KIILIEFPVVDPTFL 485
 QY 510 PGIILQKESVSPVSWKSGSKHSGKFWKALRLALPLRSU 549
 DB 466 POSLQLKSHRVLKKAKADKSLSYNSRFMKNLLIYMPAKTV 525

RESULT 12
 US-10-011-548-32
 Sequence 32, Application US/10011548
 Publication No. US20030055218A1
 GENERAL INFORMATION:
 APPLICANT: Timans, Jacqueline C.
 Debetts, Johannes Eduard Maria
 Antonius
 Bazar, J. Fernando
 Kastelein, Robert A.

TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods

NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/011,548
 FILING DATE: 22-Oct-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/173,151
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-Nov-1997
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-Mar-1998
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-Apr-1998
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-Aug-1998
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-Mar-1998
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 852-9196
 TELEFAX: (650) 496-1200
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 555 amino acids
 TYPE: amino acid
 STRANDEDNESS: No.
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US-10-011-548-32

Query Match 13.5%; Score 496; DB 9; Length 555;
 Best Local Similarity 26.4%; Pred. No. 1.2e-31;
 Matches 155; Conservative 109; Mismatches 230; Indels 94; Gaps 26;

QY 6 CVSLYFYGLQSDASERCDMDGLDTRKQIOVFEDEPARIKCPLFEHLKFNSTASTASAG 65
 DB 26 CVICNVF-----VLAGEPFAISCPV-----ITLPLMHS-D 54
 QY 66 LTLWYTRDRLDEEPINFLPENRISKEKDVLMFRPTLLNDTGNVTCMLRNTTYSKV 125
 DB 55 YNLTWY--RNGSNM--PITTE-RRARIHQKGLMFTPALLEDGLYECEVRSINRSKOK 109
 QY 126 APFLVVOKDS--CFNSPMKLPVHKLYIEVGQRTCPNVDDGY-FPSSVKPTITWYMGCY 182
 DB 110 IINLKVNDGCLPENGSK--YDQIVKSANAGKILCPDLNFPDEBNINPEIHWYCKE 167
 QY 183 K-IQNFNNVIRPGM-LSPILIALISNNGNYTCVVTYPENGRTPHLTRLITVKKVSGSPKN 239
 DB 168 SGFLEDKRLVLABGEMAILILNVTIQDKGNVTCMVVITYMGKOVNVSRTNMLRYVESPLK 227
 QY 240 AVPVVHSPNDVVEKEPEBELLPCTV--YFSLMDSRNEVMTIDGKKPDITITDV 296
 DB 228 MRPEPTV-PNNNTI-EVELGSHVVMBCNVSSGVYGLL-----PYWQVNDDEDVD--SFDS 277

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QY 297 T-----INESISHTREDETRITQILSIKVTSEDLKRSYVCHARSAKGEVAKAKVKOKV 351
DB 278 TYREGEYEEGMPIGAVSGTK-----FNISEVKLADYAKFPCHRTYDSQERTSYIKLEH-- 332
QY 352 PAPRYVELACGATVLLVILVYHYVWLEMTFYRA--HFGDEITLLOKERTDIYV 409
DB 333 PYONIRGYILGGISILIFLLILVYIKIFKIDIVMYRSSCHPLLGKRVSDKIDAVY 392
QY 410 SYARNAE-----EEFVLLTLRGVLENEBFGYKLCIFDRDLSPGANTVEAVFDFIORSRM 464
DB 393 LIPKRNESCIISSDIALKILPEVLEROCGYNLPIFGKNDLAGEAVIYDTEKIHOSRYV 452
QY 465 IVVLSP-----DYTEKSIISMLEFKLGVMCONSITATLIYVEYRPLE---HHPGIL 513
DB 453 IILVEPSCYGILEDASEHLAV---YVALIQDGI--KILILELEKIEDYANMPEBESIK 506
QY 514 QLKESISFVSWKG---EKSHSGSKTKWKALRLALPLRLSLASGSMNES 558
507 YVOKYGAIRMTGDFESERSHASTRFMKVKVRVMPSPKSHSGFHLIS 554

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RESULT 13

US-10-011-548-30

Sequence 30, Application US/10011548
 Publication No. US20030055218A1
 GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
 Debets, Johannes Eduard Maria

Antonius
 Sana, Theodore R.
 Bazan, J. Fernando
 Kastelein, Robert A.

TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSER: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,548
 FILING DATE: 22-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

* APPLICATION NUMBER: 09/173,151
 FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-NOV-1997

APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998

APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998

APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998

APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998

APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 852-9196
 TELEFAX: (650) 496-1200

```

/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 576 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: No. US20030055218A1 Relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-011-548-30

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Query Match 13.2%; Score 484.5; DB 9; Length 576;
Best Local Similarity 25.8%; Pred. No. 1.1e-30;
Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;

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QY 34 QIQVPEDEPARI-----KCPLEHFLKFNYSHTASHAGLTIYWRTRDRLDE 81
DB 21 EIDVCTEYFNQIVLFLSVNEIDIRKCPITPNKH-----GDITIIW---KNDST 67
QY 82 PINFLPENRISKEKDVLFRLPLNDTGNNTYCMLENTYCSKVAPELVOKDS--CFN 139
DB 68 PISAD-RDSRIHQONHLMFVPAKVEDSGYICVANSYCLKTKVTYVLENDPGLCTS 126
QY 140 SPKLPVHKLYIEYGIQRTCPNVDGF--PSSVKFTIYMGCIYQNFNNYIPGQML 197
DB 127 TOATFP-QRLHIA-GDGSIVCEPV--SYFDENNELPEVOMYKNC-KPLLDNVSFPGVD 182
QY 198 SFLLALIS--NNGNTYCVTYPENGRFHLTRTLTVKVGSPNNAVPYTHSPNDHYVE 255
DB 183 KLVNRVAEHHGDYICRMSYFRGQVPTVRIQPTIDENKRD-RVILSPNNEFTI-E 240
QY 256 KERSEELIPICTYVFSPLNDSRNEVMTIDGKKPDDITIDVTINES-----ISHRT 307
DB 241 ADPGSMIQLICVNTGQF---SDLVYWKNGS-----EIEKNDPLAEDYQVHEPST 293
QY 308 EDE-TRTQILSIKVTSEDLKRSYVCHARSAKGEVAKAKVKOKVAPRYVELACGFA 366
DB 290 KKKYTLITLTIINISEVKSQYRYPFICVAKNT--NIFESAHVQIYVPPFKYVLLIGFII 347
QY 367 TYLVAVITLIVYHYVWLEMTFYRAHFG--TDETILDGEXYDIYVYARNAE-----E 418
DB 348 LTAATVCCVCYIKVFPKVDILVMWRDSCSGFLPSKASDGTAYAILIYPTLGESEFSDLD 407
QY 419 EFVLLTLRGVLENEBFGYKLCIFDRDLSPGANTVEAVFDFIORSRMIVLSPD----- 471
DB 408 TVFKLLPEVLESCQFYKLFYGRDDYGEPTIEVNNVKSRLIILINDMGFSWL 467
QY 472 -YVTEKSIISMLEFKLGVMCONSITATLIYVEYRPLE--HHPGILQ-LKESVSFVSWKG- 526
DB 468 GGSSEQIAMI---YVALIQDGI--KIVLLELEKIDYEKMPDSIQFIKQKHGVCWISGD 521
QY 527 --EKSHSGSKTKWKALRLALPLRLSLASGSMNESCSQSQSDISLDHYQRRSRRL 577
DB 522 FQBRPOSAKTRFKMLRYQMPAQRSS-----PLSKRLTLIDPVRYDKEXL 567

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RESULT 14

US-09-731-175-4

Sequence 4, Application US/09731175
 Patent No. US20020098168A1
 GENERAL INFORMATION:

APPLICANT: Glorioso, Joseph C.
 Evans, Christopher H.
 Robbins, Paul D.

TITLE OF INVENTION: Gene Transfer for Studying and Treating
 a Connective Tissue of a Mammalian Host

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/731,175
FILING DATE: 05-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/924,777
FILING DATE: 2000-01-31
APPLICATION NUMBER: US 07/963,928
FILING DATE: 20-OCT-1992
APPLICATION NUMBER: US 08/027,750
FILING DATE: 08-MAR-1993
APPLICATION NUMBER: US 08/183,563
FILING DATE: 18-JAN-1994
APPLICATION NUMBER: US 08/381,603
FILING DATE: 27-JAN-1995
APPLICATION NUMBER: US 08/567,710
FILING DATE: 05-DEC-1995
APPLICATION NUMBER: US 08/685,212
FILING DATE: 23-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 018484-002280US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-731-175-4

Query Match 13.2%; Score 484.5; DB 10; Length 576;
Best Local Similarity 25.8%; Pred. No. 1.1e-30;
Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;

QY 34 QIQVFEDEPARI-----KCPFEHFLKNSTANASAGITLIWYTRDRIE 81
DB 21 EIDVCTEPNOIVFLSVNEIDIRKCPLETPNKM-----GPTIIMY-----KNSKT 67
QY 82 PINRLPENRISKEDVLMFRPTLLINDGNVTCMLRNTTYSKVAFLPVQKOS--CFN 139
68 PISAD-RDSRHHQNEHLMFPAKVEDSGYYCIYRNSITCLTKRVYTVLENDPLGYS 126
QY 140 SPMKLPVHKLYIEVGIOKITPNVDGYE--PSVVPRTITWGCYKIONFNNVJPEGNAL 197
DB 127 TOAFVP--QRLHIA-GDGLVCPYV-SYFKDENNELPEVOWKNC-KPLLLNVSPFGKD 182
QY 198 SFILALIS--NNGNVTCTVTPENGRTFLRLTLTKVAVGSPKAVPVYHSPNDHAYVE 255
DB 183 KLVARNVAEERGDYICMSYTFRGKQVPYTRVIOFITIDENKRD-RVVIISPRNETI-E 240
QY 256 KEPEEBLIPCTVVFSPFLMDSRNEVWMTIDGKKPDITIDVTINES-----ISHRT 307
DB 241 ADPSMTOLICNVGTGF-----SDLVYWKNGS-----ELEMNDPLAEDYQFHEHST 289
QY 308 EDE-TRTOILSIKVTSEDLKRSYVCHARSAGEVAKAKVQKVPARYVELAAGFGA 366
DB 290 KRKYTLITLTLNISSEKVSQFYRYPVICVKNY--NIFESAHVOLIVPDPFKVILGFTII 347
QY 367 TVLLVLLIVVYVYVWLEMTLFYRAHFG--IDETLLDKEVDIYVSARNAER-----E 418
DB 348 LTAIVTCCVCVCIYKVFQVIVLWYRDSGSGPLPSKASDKTDAYLILYKTLGEGSFSOLD 407
QY 419 EFVLLTLRGVLENEFGYKLCIFDRDLSLPGNIVEAVDFIQRSRRIIVLSPD----- 471

DB 408 TTFVKLLPEVLBGQFGYKLFYGRDDYVGEDTIEVTNENVKSRRLIILIVDMGFSWL 467
QY 472 -YVTEKISLMEKLGAMCONSIATKLIYERAPLE--HPHPILO-LMESVFSVMKG- 526
DB 468 GGSSEQIAL---YNALIOEGI--KIVILLEKIDYERMPDSIOPIKQKHGVCMSGD 521
QY 527 --EKSKHSGSKFWKALRLALPLRLSLASSGWNESCQSQSDISDHYORRRSRL 577
DB 522 FQERPOSATRFWKNLRYQMPAQRSS-----PLSKRLITLDPVADYKEL 567

RESULT 15
US-10-011-548-29
Sequence 29, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Debets, Johannes Eduard Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kaetelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030055218A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-011-548-29

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:50:35; Search time 47 Seconds

(without alignments)
1405.199 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVSLYFGILQSDA.....SALALHFTDLSNNDFYLL 687

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2327.5	63.4	570	2 A57535	interleukin-1 recep
2	486	13.5	555	2 T01526	interleukin-1 rece
3	493.5	13.5	590	2 T56526	interleukin-1 rece
4	484.5	13.2	576	2 A32604	interleukin-1 rece
5	478	13.0	567	2 S29498	lymphocyte antigen
6	444.5	12.1	562	2 G02426	interleukin-1 rece
7	424.5	11.6	569	2 A36187	interleukin-1 rece
8	302	8.2	416	2 S33473	interleukin-1 rece
9	256	7.0	247	2 S42633	interleukin-1 rece
10	252	6.9	398	2 S17428	interleukin-1 rece
11	229.5	6.3	328	2 S30444	ST2 protein - huma
12	220	6.0	336	2 A42632	ST2 protein - huma
13	189	5.2	326	1 MMV215	interleukin-1 beta
14	189	5.2	326	2 T37450	interleukin-1 beta
15	189	5.2	5175	2 T20992	hypothetical prote
16	189	5.2	5198	2 T43290	hypothetical prote
17	179	4.9	7962	2 T38346	hemilectin precurs
18	173	4.7	290	2 P42527	B16R protein - hu
19	165.5	4.5	259	2 JCT109	ST2V protein - hum
20	165	4.5	169	2 T51803	type I interleukin
21	159	4.3	1097	2 A29943	Toll protein precu
22	151.5	4.1	243	2 S11226	MyD88 protein - mo
23	148.5	4.0	1260	1 S05479	neural cell adhesi
24	147.5	4.0	786	2 T08664	Toll protein-like
25	144.5	3.9	812	2 B42632	cell adhesion mole
26	144.5	3.9	932	2 A42632	cell adhesion mole
27	143.5	3.9	1259	2 A43425	Bravo/NF-CAM cell
28	140.5	3.8	6642	2 T29757	protein UNC-89 - C
29	140	3.8	1033	2 S19247	cell adhesion prot

30	137.5	3.7	818	2 UC4058	fibroblast growth
31	137.5	3.7	1389	2 T13852	gene wheeler prote
32	136	3.7	1306	1 S68235	myosin-light-chain
33	135.5	3.7	1257	1 A41060	neural cell adhesi
34	134.5	3.7	765	2 A42632	cell adhesion mole
35	134	3.7	824	2 S24108	protein-tyrosine k
36	134	3.7	1268	1 A39640	neural cell adhesi
37	133.5	3.6	1385	2 T13887	clt protein - fru
38	133	3.6	423	1 EHMS	Ig epsilon chain C
39	133	3.6	1333	2 T18875	receptor tyrosine
40	133	3.6	1896	2 T08851	Down syndrome cell
41	131.5	3.6	1259	2 S36126	neural cell adhesi
42	130.5	3.6	799	2 S18209	fibroblast growth
43	130	3.5	2051	2 T30938	receptor tyrosine
44	129.5	3.5	964	2 T15746	hypothetical prote
45	129.5	3.5	1091	2 A58532	glial cell membran

ALIGNMENTS

RESULT 1

A57535 interleukin-1 receptor accessory protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #ext_change 17-Mar-2000

C/Accession: A57535

R/Greenfeder, S.A.; Nunes, P.; Klee, L.; Labow, M.; Chizzonite, R.A.; Ju, G.

J. Biol. Chem. 270, 13757-13765, 1995

A/Title: Molecular cloning and characterization of a second subunit of the interleukin-1 receptor

A/Reference number: A57535; MUID:95293970; PMID:775431

A/Accession: A57535

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-570 <GR>

A/Cross-references: GB:X85999; NID:9887520; PID:CAA5999.1; PID:9887521

A/Superfamily: interleukin-1 receptor type I

C/Keywords: transmembrane protein

Query Match	Score	Length	DB 2	Length	DB 2	Length	DB 2	Length	DB 2
Best Local Similarity	75.9%	Pred. No.	4.4e-168	Matches	429	Conservative	66	Mismatches	55
QY	1	MTLWCVSLYFGILQSDASERCDMDGIDYMQIOVFEDEPARIKCPLEHFLKENVST	60						
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QY	61	AHSAGLTLIWMYTRQDRDLEBPINFRLPENRISKEDVLMFRFTLNDGTGNTQMLRNTT	120						
DB	61	AHSSGTLTLIWMYTRQDRDLEBPINFRLPENRISKEDVLMFRFTLNDGTGNTQMLRNTT	120						
QY	121	YCSKVAFLPLAVVOKDSCFNPMKLPVHKLYIEGIORITCPNVGYPSSVKTITWYMG	180						
DB	121	YCSKVAFLPLAVVOKDSCFNPMKLPVHKLYIEGIORITCPNVGYPSSVKTITWYMG	180						
QY	121	YCSKVAFLPLAVVOKDSCFNPMKLPVHKLYIEGIORITCPNVGYPSSVKTITWYMG	180						
DB	121	YCSKVAFLPLAVVOKDSCFNPMKLPVHKLYIEGIORITCPNVGYPSSVKTITWYMG	180						
QY	181	CYVIOFNPNVPIRGKMLSTLALISNNGNTCVVTPENGRTFLRLTIVKVGSPKNA	240						
DB	181	CYVIOFNPNVPIRGKMLSTLALISNNGNTCVVTPENGRTFLRLTIVKVGSPKNA	240						
QY	181	CYVIOFNPNVPIRGKMLSTLALISNNGNTCVVTPENGRTFLRLTIVKVGSPKNA	240						
DB	181	CYVIOFNPNVPIRGKMLSTLALISNNGNTCVVTPENGRTFLRLTIVKVGSPKNA	240						
QY	241	VPPVHSPNDHYVEKEPSEKLLIPCTVYFSLDNRNEMWTIDGKKDDITIDVTINE	300						
DB	241	VPPVHSPNDHYVEKEPSEKLLIPCTVYFSLDNRNEMWTIDGKKDDITIDVTINE	300						
QY	241	VPPVHSPNDHYVEKEPSEKLLIPCTVYFSLDNRNEMWTIDGKKDDITIDVTINE	300						
DB	241	VPPVHSPNDHYVEKEPSEKLLIPCTVYFSLDNRNEMWTIDGKKDDITIDVTINE	300						
QY	301	SIHSSTEDETRTQIISIKVTSEDLKRSYVCHASAKGAVAKAVKQVAPRYVEL	360						
DB	301	SIHSSTEDETRTQIISIKVTSEDLKRSYVCHASAKGAVAKAVKQVAPRYVEL	360						
QY	301	SIHSSTEDETRTQIISIKVTSEDLKRSYVCHASAKGAVAKAVKQVAPRYVEL	360						
DB	301	SIHSSTEDETRTQIISIKVTSEDLKRSYVCHASAKGAVAKAVKQVAPRYVEL	360						
QY	361	ACGFGATVLLVLLIVVYVWVLEMLFYRAHGTDETLIDGEXYIVSYANAEER	420						
DB	361	ACGFGATVLLVLLIVVYVWVLEMLFYRAHGTDETLIDGEXYIVSYANAEER	420						
QY	361	ACGFGATVLLVLLIVVYVWVLEMLFYRAHGTDETLIDGEXYIVSYANAEER	420						
DB	361	ACGFGATVLLVLLIVVYVWVLEMLFYRAHGTDETLIDGEXYIVSYANAEER	420						
QY	421	VLLTGLVENERGYLCTFDRDSLPGANTVEAVPFIORSRMIVLSPDYTESISM	480						
DB	421	VLLTGLVENERGYLCTFDRDSLPGANTVEAVPFIORSRMIVLSPDYTESISM	480						
QY	421	VLLTGLVENERGYLCTFDRDSLPGANTVEAVPFIORSRMIVLSPDYTESISM	480						
DB	421	VLLTGLVENERGYLCTFDRDSLPGANTVEAVPFIORSRMIVLSPDYTESISM	480						

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Db 421 VLLTLRGVLENEFGYKLCI PDRDSLPGGI VTDETLSTFIQSRLLVLSPPVYLQGTAL 480
Qy 481 LEFLKGVMCQNSIATK---LIVEYRPLEHPHGIQLQKES---VSFVSKGSKXHG 533
Db 481 LELKAGL---ENMASRGNIIVLVQYKAVKDMK---VKELKRAKTLVTVIKWGEKSKYPO 535
Qy 534 SKFWALRLALPIRLSLSSAGSNNES 558
Db 536 GRFWKQLQVAMPVK---SPRWSSN 557

RESULT 2
J01526
interleukin-1 receptor I precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 29-Sep-1999
C/Accession: J01526
R/Guid: S.; Heguy, A.; Melli, M.
Gene 111, 239-243, 1992
A/Title: The chicken IL-1 receptor: differential evolution of the cytoplasmic and extra
A/Reference number: J01526; MUID:92175529; PMID:1531799
A/Cross-references: GB:M81846; NID:g212206; PIDN:AAA48924.1; PID:g212207
Molecule type: mRNA
Residues: 1-555 <GUI>
Query Match 13.5%; Score 496; DB 2; Length 555;
Best Local Similarity 26.4%; Pred. No. 1.7e-29;
Matches 155; Conservative 109; Mismatches 230; Indels 94; Gaps 26;
Qy 6 CVVSLYFGIIGDSERCDWGLDTMQIOVFDEPARICPLEHFLKKNYSTAHSG 65
Db 26 CVITCNP-----VLGEPRALISCPV-----ITLPMHS-D 54
Qy 66 LTLVYWRQDRLPEPINFRLPERNISKEKQVLFWRPTLLNDTNGYTCMLNNTYCSKV 125
Db 55 YNLTVY--RNGSNM--PITTE--RRARIHQKGLMFI PALEDSGLVCEVRSLSRQK 109
Qy 126 APFLEVQKDS--CFNSPKLPHKLYIEYGIQITCPNVQY--FPSSVKPTITTYMGCY 182
Db 110 IINLVKFKNDGLCFNGEMK--YDOIIVSANAAGKIICPLENFKQEDNINDEIHWECK 167
Qy 133 K--IQNFNNVIREGN--LSFLALISNNQNTCVVTPENGRTFLHTRTLTVKVGSPKN 239
Db 168 SGFLDDKRLVLAEGRNALILNVTTIODKGNVTCRVVITYMGQVNSHTMLNEVESPLK 227
Qy 240 AVPPYIHSFNDVVEKEPGEELIPCTV---YFSLMDSRNEVWMTIDGKKPDDITIV 296
Db 228 MRPEPIY--PNNTI--EVELGSHVMECAVSSGVGL-----PYQVNDDEVD--SFDS 277
Qy 297 T-----INESIHSRTDEDTQTQIISIKKVTSEDLKRSYVCHASAKAEVAKAVKOV 351
Db 278 TYREOFYEEMPHGLAVSGTK--FNISEVKLKDYAVKFCFIYDSOEFTSYILEH-- 332
Qy 332 PAPRTVELAGRGATVLLVLLIVVHYVLMELVLYRA--HFGTDETLIDGKEXDYV 409
Db 333 FVQNIIRGVIIGGISILIFLILVYKIFKIDIVLMTRSSGHPPLGKKSVDGKIYDNYV 392
Qy 410 SYARNAE-----EEEFVLLTLRGVLENEFGYKLCIFDSDLSFGCNTVEAVDFIORSRM 464
Db 393 LYPKRESGLVSSDIFALKILPEVLERQGVNLFIFGRNDLAGAIVDVTDEKIHQSRV 452
Qy 465 IYVLSP-----DYTEKSIISMLEFLKGVMCQNSIATKLIVERYPLE--HPHGI 513
Db 453 IILVPEPSCYGILBEDASKEHLAV---YNALIDGI--KILLILEKTEIDYANPESIK 506
Qy 514 QKESVYFVSMKG---EKSHSGSKFWKALRLALPIRLSLSSAGSNNES 558

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Db 507 YVQKYGAIKMTGDFSESRSHSASTRFKVKVRYHMPERSKSSSGFHLIS 554
Qy 507 YVQKYGAIKMTGDFSESRSHSASTRFKVKVRYHMPERSKSSSGFHLIS 554

RESULT 3
I56526
interleukin 1 receptor type I - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 29-Sep-1999
C/Accession: I56526
R/Hart, R.P.; Liu, C.; Shadiack, A.M.; McCormack, R.J.; Jonakait, G.M.
J. Neuroimmunol. 44, 49-56, 1993
A/Title: An mRNA homologous to interleukin-1 receptor type I is expressed in cultured
A/Reference number: I56526; MUID:93266794; PMID:7684399
A/Accession: I56526
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-590 <RES>
A/Cross-references: GB:M95578; NID:g451305; PIDN:AAA16196.1; PID:g451306
C/Superfamily: interleukin-1 receptor type I
C/Keywords: cytokine receptor

Query Match 13.5%; Score 493.5; DB 2; Length 590;
Best Local Similarity 26.5%; Pred. No. 2.9e-29;
Matches 153; Conservative 105; Mismatches 230; Indels 89; Gaps 25;
Qy 47 CPLEFHLKRYSTAHNAGLTLVYWRQDRLPEPINFRLPERNISKEKQVLFWRPTLL 106
Db 60 CPLEPNEH-----GGTIIWY---KNDSTPIASD--KDRHIQNHLMFVPAKM 105
Qy 107 NDTGNYTCMLNNTYCSKVAPFLEVQKDS--CFNSPKLPHKLYIEYGIQITCPNVQY 164
Db 106 EDSGYTICIMNSTYCLKTKITMSVLENDPGLCTNQAS--IQRHVA--GGSIVCPYLD 163
Qy 165 GYF--PSSVKPTITTYMGCYKIQNFNNVIREGN--LSFLALISNN-----GNTYCVVY 216
Db 164 -FFDQENNELPKVQYNGCKLP-----LDDGNFFGFKMLMNNVVAEHRGNTYCRYS 217
Qy 217 PENGRTFLHTRTLTVKVGSPKNAVPPYIHSFNDVVEKEPGEELIPCTVYSSFLMS 276
Db 218 TYQCKQYVPRVIFITIDSKRD--RPVMSPRHEM--EADPGSTIOLICVTVQF--- 271
Qy 277 RNEVWMTIDGKKP--DITIDVTINESISH--SRTERDTQIISIKKVTSEDLKRSYVCHA 334
Db 272 TDLVYMKNGSEIEMDPIAEDYQFLEHPSAKKTLITLANSYVKSQYRPRIFCV 331
Qy 335 RSAGGVAKAKVQKVPARYVELACGFATVLLVLLIVVHYVLMELVLYRAHFG 394
Db 332 KNT--HILETAHVLLVVPDPFKVYLLGFFALPTATAVFCACIYKVPKVDIVLWYRDCS 389
Qy 395 --TDETIDGKEXDYIYSYARNAE-----EEFVLLTLRGVLENEFGYKLCI PDRDSL 446
Db 390 DFLPRKASDGTAYAVLYPPTYEGSPAYLDTVFPLLPVLELGGQFQYKLPICGRDYV 449
Qy 447 GGNTEAVFDIORSRMIVVLSPPYVTEKSIISMLEFK--LGVMCQNSIATK-----TK 496
Db 450 GEDTIEVTENVAKSRKLIILVVD-----MGSBCLOQSSSEQAIYDALIREIK 501
Qy 497 LIVEYRPLEHPHGIQLQKESVFSV-----WKG---EKSHSGSKFWKALRLALPL 546
Db 502 IILLELEKIQYVE---KMPESTQFIKQKHGALCMGDFEKRPQSAKTRFWKNIRAYQMDA 557
Qy 547 RSLSSAGSNNESCSQSDISLDHYQRRSRKAKEPEL 583
Db 558 QRRS-----PLSKHMLTLDPVLTDEKQLQAEHTL 587

RESULT 4
A32604
interleukin-1 receptor precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 29-Sep-1999
C/Accession: A32604

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R.Sims, J.E.; March, C.J.; Cosman, D.; Widmer, M.B.; MacDonald, H.R.; McManan, C.J.; Gru S.K.
 Science 241, 585-589, 1988
 A:Title: cDNA expression cloning of the IL-1 receptor, a member of the immunoglobulin su
 A:Reference number: A32604; MUID:88290679; PMID:2965618
 A:Molecule type: mRNA
 A:Accession: A32604
 A:Residues: 1-576 <SIM>
 A:Cross-references: GB:M20658; GB:M29752; NID:g198300; PIDN:AAA39279.1; PID:g309399
 C:Superfamily: Interleukin-1 receptor type I
 C:Keywords: cytokine receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-576/Product: interleukin-1 receptor #status predicted <INT>
 F:339-359/Domain: transmembrane #status predicted <TM>
 F:46-99,145-199,251-315/Disulfide bonds: #status predicted
 F:63,103,174,236,252,266,300/Binding site: carbohydrate (Asn) (covalent) #status predicted

Very Match 13.2%; Score 484.5; DB 2; Length 576;
 est Local Similarity 25.8%; Pred. No. 1.4e-28;
 Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;

QY 34 QI QV EDEDEARI-----KCPLEHFLKFNYSRAHAGLILVYWRQDDLEE 81
 DB 21 EIDVCTEYENQIVLFLSNEIDIRKCPLEPNKMH-----GDTIIYV---KNDSKT 67
 QY 82 PINFLPERISKEKDVLFRRPTLNDTGNVTCMLNTTYCSKVAPELVEVQDS--CFN 139
 DB 68 PISAD-RDSRIHQNHLMFVPAKVEDSGYTCIVANSTYCLTKTKVTVVLENDPLGLCS 126
 QY 140 SPMKLPVHKLVEYGIQRTICPNVDYF--PSSVKPTITWMCYKIQNFNNVPRGMNL 197
 DB 127 TQATFP-QELHIA-GDGSIVCFYV-SYFDENNELPEVQMYKNC-KPLLDNVSPFGVND 182
 QY 198 SFLIALIS--NNGNTCVVTPENKRTFHLTRLYKAVGSPGNAPPIHSHNDVVE 255
 DB 183 KLLVRNVAEHHGDYICRMSYTERGQYPTVRIQPTIDENKRD-RPVLSPRNETI-E 240
 QY 256 KERGSEELLPTCYVFSFLMDSRREVMWITIDGKKPDDITDVTINES-----ISHSRT 307
 DB 241 ADPGSMIQLICVNTGQF---SDLVYWKMGNS-----EIEENDPLAEDYFVHPST 289
 QY 308 EDE-TFTQILISIKRTVSEDLKRSYVCHASAKGEVAKAKVKQVAPRYVELACGPGA 366
 DB 290 KKKYTLITLITNISSEVKSQFRYPFICVVKNT--NIPESAHVQIIVPDPKXVLLCGFII 347
 QY 367 TVLLAVITLVVHVYVLEWLFYRAHFG--TDFTIIDGKRYDIYVSARNAE-----E 418
 DB 348 LTAIVCCVCYIVFVVDIVLWYTRDSCSGFLPSKASDGKTYDAVYIIPKTLGSGFSDDL 407
 QY 419 BFLVLTLRGVLENERFGYKLCIPDRSLPGCNTVEAVFDFIORSRMIVLSPD-----471
 DB 408 TTFPKLLEVLBSQFGYKLPFYGRDYGEDTIEVTNENKSKSRLLITLIVRDMGFSWL 467
 QY 472 -YVTEKSIEMLEFKLVCMCONSIATKLIIVERAPLE--HPHPILO-LKESVFSVMKG- 526
 DB 468 GGSSEQIMAI-----VVALQDEGI--KIVLLELEKIDYEMKPSISQPIQKHGVICMSGD 521
 QY 527 --EKSHSGSKFKALRLALPLRLSASSGKNSSCSQSDISLHVQRRSRRL 577
 DB 522 FDRPQSAKTRFWKRLRYQMFAQRSS-----PLSKHRLITLDPVADTDEKL 567

RESULT 5
 S29498
 lymphocyte antigen ly84 precursor - mouse
 N:Alternate names: 38.5K T1 glycoprotein; ST2L protein
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #ext_change 01-Dec-2000
 C:Accession: S29498, A33541, S17657, S07054
 R:Yanagisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tomioka, S.
 FEBS Lett. 318, 83-87, 1993
 A:Title: Presence of a novel primary response gene ST2L, encoding a product highly simi
 A:Reference number: S29498; MUID:93170492; PMID:7916701

A:Accession: S29498
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-567 <YAN>
 A:Cross-references: EMBL:D13695; NID:9286100; PIDN:BAA02854.1; PID:9286101
 R:Klemmer, R.; Hoffmann, S.; Werenkold, A.K.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989
 A:Title: Serum- and oncoprotein-mediated induction of a gene with sequence similar
 A:Reference number: A33541; MUID:89345536; PMID:2527364
 A:Accession: A33541
 A:Molecule type: mRNA
 A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA', <KLE>
 A:Cross-references: GB:M24843; NID:9201103; PIDN:AAA40160.1; PID:g201104
 R:Tomioka, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.
 Biochem. Biophys. Acta 1090, 1-8, 1991
 A:Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal
 A:Reference number: S17657; MUID:91355215; PMID:1832015
 A:Accession: S17657
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA', <TOM>
 A:Cross-references: EMBL:X60184; NID:954200; PIDN:CAA42742.1; PID:g54201
 R:Tomioka, S.I.
 FEBS Lett. 258, 301-304, 1989
 A:Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is high
 A:Reference number: S07054; MUID:90092495; PMID:2532153
 A:Accession: S07054
 A:Molecule type: mRNA
 A:Residues: 1-328, 'SKECPSHIA', <TO2>
 A:Cross-references: EMBL:Y07519; NID:g55517; PIDN:CAA6812.1; PID:g55518
 A:Note: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator
 A:Genes: ST2
 C:Genes: ST2
 A:Map position: 1
 A:Functions: 27/1, 97/2, 155/3, 210/1, 233/1, 280/2
 C:Superfamily: Interleukin-1 receptor type I
 C:Keywords: glycoprotein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-337/Product: ST2 protein #status predicted <MAY>
 F:60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 13.0%; Score 478; DB 2; Length 567;
 Best Local Similarity 25.9%; Pred. No. 4.1e-28;
 Matches 163; Conservative 105; Mismatches 227; Indels 134; Gaps 28;

QY 4 LW--CVSLYFGLIOSDSERCDWGLDTMRQIOVFEDDEPARIKCPLEHFLKFNYSRA 61
 DB 9 LVALALITLPMY-LTVTESK--SSWGL-----ENBALIVRCP-----QKGRST- 49
 QY 62 HSAGLTLVYWRQDDLEEPINFLPERISKEKDVLFRRPTLNDTGNVTCMLNTTY 121
 DB 50 ----YVEKITYS---DTNESIPTQ-KRRRITFVSRRRLKFLPARVDSGIYACVIRSPUL 100
 QY 122 CSKVAPELVEVQDSCFNSPMKLPVHKLVEYGIQF-----ITCPNVDSGFPSVSKFT 174
 DB 101 NKGVLNVTIHKKRPSCNIPD-----YIMYSTVAGSDKNFETICTPTIDLY---NWTAP 150
 QY 175 ITTYMGCYKIQF-----FNNVIRPGANLSTLIALISNNGNTCVVTPENKRTF 223
 DB 151 VQWFKRCKALOEBRFRHRSYLFIDVNTD-----DEGYTCQFTHAENGTVY 198
 QY 224 HLTRTLTVKVGSPKNAVPPVISHPNDAVYKEKPEBELLIPCTVYFS-----FLMDSRNE 279
 DB 199 IYTAIRSLFVEBEKFSMPVITNPPIHNM-EVEIKRPSIACSACFGGSHFLAD-----253
 QY 280 VVMTIDGKKPDDITDVTINESISHRTDE-----TRTQILSIKKVTSSEDLK 327
 DB 254 VLM-----QINKTVVGNGBARIQEBEGRSSSSNDMDCLTSVLRITGVTEKDS 303
 QY 328 RSYVCHASAKGEVAKAKVKQVAPRYTV-ELAGFGATVILVYVHVYVLEWLF 386
 DB 304 LEYDCIALMLHGMIRRTIRLRKQPIDHSIYIYVAGCSLLMFNVLVILKVFWEIVA 363

QY 387 LEYRAHGTDETLIDGKEYDIYVSAR-----NAEERFVLLTLRGVLENGEYKLC 438
 DB 364 LFMEDIVTPKTRNDGLKIDYIYIPVYFGSAAGTMSVEYFVHTTLPDVLENGKGYLDC 423
 QY 439 IFPRDSLPGANTVEAVEFDIORSRMTIVLSP-----DYTEKSIISMLFEKLGVMCONS 492
 DB 424 IYGRDILLPGDDAATVAVSSISONSRRQVFVLAIPHMMHSKEFAVEDEIAL-----HSLILQNN 479
 QY 493 IATKLYVEYRPL-EHHPGILQIKESVSF-----VSWKGE--KSKHS-GSKFPMALR 541
 DB 480 --SKVILIEHEPGLGEARLYQVGLDLSIOLHVKIIGITIKMRBDHVADKOSISKFMKIVR 537
 QY 542 LALPL-RSLSSAGSMNSCSSOSDISLDH 569
 DB 538 YQMFVPERASKTASVAAPLSGACLDLKH 566
 RESULT 6
 G02426
 interleukin-1 receptor-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999
 Accession: G02426
 Jovenberg, T.W.; Crowe, P.D.; Liu, C.; Chalmers, D.T.; Liu, X.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: H01239
 A:Accession: G02426
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-562 <LOV>
 A:Cross-references: EMBL:U49065; NID:g1236078; PIDD:AA5337.1; PID:g1236079
 C:Superfamily: Interleukin-1 receptor type 1
 Query Match 12.1%; Score 444.5; DB 2; Length 562;
 Best Local Similarity 25.5%; Pred. No. 1,46-25;
 Matches 148; Conservative 119; Mismatches 236; Indels 77; Gaps 26;
 QY 2 TLIMCVSLFYTGILQSDASERCDDMLTKROIQVFEDEPARIKPLFEHLEKNSTA 61
 DB 3 SLLLCGLSI--ALPLSVTDGCKD--IFMKNEILSASQFPAFNC-----TFPPI 47
 QY 62 HSAGLTILWTRQDRDLDEEPINFLPENRISKEQDVMPFPTLLNDGNTYCMRLNTTY 121
 DB 48 TSGEVSATWY---KNSKIPVS-KIIOSRIHODETWILFLPMKMGDSGVYQCVYKGRDS 102
 QY 122 CSKVAFLPEVVQKDSCFNSPMKLP---VHKLYIEYG-IORITCPNVGYFPSS-VKPTI 175
 DB 103 CHRILHNVLTVEKIMCDTISIGLPLNLSDEYKQILHLGKDSLTG--HLHFPKSCVLGPI 159
 QY 176 TWYMGCKYIQNFNNVIEGKMLSFILALIS--NNGNYTCVVTYPENGRTFHLTRLTVKVS 233
 DB 160 KMYDNCIEIKERPTV--LETLLVSNVSAEDRGVACQAILTHSGQYEVLMNGITYSI 216
 QY 234 V--GSPNAVPEVISHPDHVVYEKEPGEELLIPCTVYFSLMDSRNEVMTITDCKPDD 291
 DB 217 TERAGYGGSVPKIY-PRNHSI-EVQLGSTIYVDCNV--TQTKDNTLRCRKNNTLVDD 272
 QY 292 ITID-VTINESI-SH-SRTDETRTQILSIKVTSEDLKRSYVCHASAKGEVAKAKVK 348
 DB 273 YYDESKIRIEGVETHVSFRHNLTVTNITPLEVKMEDYGLPFMCAG-----VSTAYII 326
 QY 349 QKVAPRYTVELACGFATVLLVILVYVYVYVLEMLTFRAHGTDETLIDGKEYIY 408
 DB 327 LQLPAPDPRAVLLIGLALVAVAASVATYINIFKIDIVLRSASHTETTVGDLXAY 386
 QY 409 VSYARNAEER-----EEFVLLTLRGVLENGEYKLCIFPRDSLPGANTVEAVEFDIORS 462
 DB 387 VLYGPKPKHESGRHVAVDALVNLPEVLERQCGYKLFIFGRBEPGQAVANYIDENVKCR 446
 QY 463 RMIVLVSPD-----VTEKSIISMLEFKLGVMCONSIAATKLIVVEYRPLEH----DHP 510
 DB 447 RLIVIVVESIGFGLIKMLSEEOIAV-----YSALIQDGM--KVLILIELEKTEDYVMBE- 499

QY 511 GILQKESVSFVSMKG---EKSXHSKSKFWKALRLALPLR 547
 DB 500 SIQYIKKHGALRMHGDFTVSOCKMTKFMKIVRYHMPRR 539
 RESULT 7
 A36187
 interleukin-1 receptor type I precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 29-Sep-1999
 C:Accession: A36187; S06928
 R:Stim, J.E.; Acres, R.B.; Grubbin, C.E.; McMahon, C.J.; Wignall, J.M.; March, C.J.; D
 Proc. Natl. Acad. Sci. U.S.A. 86, 8946-8950, 1989
 A:Title: Cloning the interleukin 1 receptor from human T cells.
 A:Reference number: A36187; MUID:90046906; PMID:2530587
 A:Accession: A36187
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-569 <SIM>
 A:Cross-references: GB:M20658
 R:Chua, A.O.; Gubler, U.
 Nucleic Acids Res. 17, 10114, 1989
 A:Title: Sequence of the cDNA for the human fibroblast type interleukin-1 receptor.
 A:Reference number: S06928; MUID:90098789; PMID:2532321
 A:Accession: S06928
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-569 <CHU>
 A:Cross-references: EMBL:X16896; NID:g33800; PIDD:CAA34773.1; PID:g33801
 C:Genetic:
 A:Gene: GDB:111R1; IL1RA; D261473; IL1R
 A:Cross-references: GDB:125254; OMIM:147810
 A:Map position: 2q12-2q12
 C:Superfamily: Interleukin-1 receptor type I
 C:Keywords: cytokine receptor; transmembrane protein
 Query Match 11.6%; Score 424.5; DB 2; Length 569;
 Best Local Similarity 24.3%; Pred. No. 4,6e-24;
 Matches 129; Conservative 117; Mismatches 205; Indels 79; Gaps 24;
 QY 67 TLIVWTRQDRDLDEEPINFLPENRISKEQDVMPFPTLLNDGNTYCMRLNTTYCSKVA 126
 DB 54 TIITWY-----KDDSKTPVSTE-QASRIHQHCKMLFPAKEDBSGHYCVVRNSSYCLRIK 108
 QY 127 PPLEVVQKDS--CFNS---PMKLPVHKLYIEYGIORITCPNVGYF--DSSVAKPTITWY 178
 DB 109 ISAKFVENEPLCYNAQAFKQKLPV-----AGDGLVCPYME--FPKNNENELPKLOMY 161
 QY 179 MGCKYIQNFNNVIEGKMLSFILALIS--NNGNYTCVVTYPENGRTFHLTRLTVKVS 236
 DB 162 KDC-KPLLLNHSFGVNDRLIVANVAEKRGVYTGASTYVLSKQPIITRVILEPITLSE 220
 QY 237 PKNAVPEVISHPDHVVYEKEPGEELLIPCTVYFSLMDSRNEVMTITDCKPDDITIDV 296
 DB 221 NKPRFPIVSPAB--TMEVDLSQIOLICNTYQGL-----SDIAYMKMNSVIDE--DDP 272
 QY 297 TINESI---SHSRTDETRTQILSIKVTSEDLKRSYVCHASANGEVAKAKVKOKVP 352
 DB 273 VLGEDYVSVENPANKRSTLITVINISEISREFKHPFTCFANHTG--IDAAYIQLIYIP 330
 QY 353 APRTYVELACGFATVLLVILVYVYVYVLEMLTFR--AHRTDTEITIDGKEYDI 407
 DB 331 VTNFQKHM--IGICVTLVIVVCSVATYIKIFKIDIVLWRDSQYDFLPIKASDGKTYDA 387
 QY 408 VSYARNAEER-----EEFVLLTLRGVLENGEYKLCIFPRDSLPGANTVEAVEFDIORS 461
 DB 388 YIYLPKTVGSGSDCDIFPKVLPVLEKQCGYKLFITGRDGYVGBDIYEVNENVKKS 447
 QY 462 RMIVLVSPD-----VTEKSIISMLEFKLGVMCONSIAATKLIVVEYRPLEHFGIL 513
 DB 448 RRLIILIVRETSGRFVLSGSSSEEOIAM-----YNALVODGI--KVLILIELEKIDYV- 497
 QY 514 QLKESVSFVS-----WKGEKS---KHSGSKFWKALRLALPLRSLSASS 553

Db 498 KMESEIKIKQKGAIRMSGDFTQGPQSAKTRFWKVRVHMPVGRSPSS 547

RESULT 8

interleukin-1 receptor type 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999

C:Accession: S33473

R:Brictul, J.; Gatti, S.; Bartfai, T.

submitted to the EMBL Data Library, May 1993

A:Description: The rat insulinoma beta-cell line RINm5F express mRNA for the type 2 interleukin-1 receptor

A:Reference number: S33473

A:Accession: S33473

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-416 <BRI>

A:Cross-references: EMBL:Z22812; NID:G311407; PIDN:CAA80465.1; PID:G311408

C:Keywords: cytokine receptor

Query Match

8.2%; Score 302; DB 2; Length 416;

Best Local Similarity 25.3%; Pred. No. 5, 6e-15;

Matches 97; Conservative 67; Mismatches 153; Indels 66; Gaps 18;

Qy 25 DDM--GLDTRQIOVEDEPARIKCPLEFHEFLKFNSTAHSAGLTLIWTRODRLEEP 82
 Db 41 DCMFRGRDFKSELRL-EGEPVVALKCPVPH-----SDTSSSRSLT-TWKSQDSQILIP 92
 Qy 83 INFRLENRISKEKDVLMFRPTLNDTGNATYCMLENTTYSKVAFLPEVQKDSQCFNSPM 142
 Db 93 GD-----EPHVMVADDTLMLPAVQDSQTYICTFRNASHCEQMSLELKER-----NTEA 143
 Qy 143 KLPVHKLTYIEYGIQRT---CPNVDGYPSSVKKPTITWMCYKIQNFNNVIEPQNLIS 188
 Db 144 SPFLVS-VLQISALSTGTLVCPDLKEFISRTDGKIQWYK-----SILLDKNKK 194
 Qy 199 FLIA-----LISNN-----GNTCVATYBENGRTFHLTELTLYKVVGPSKNAVPIYHS 247
 Db 195 FLASGPTLLISNTSMGADGYRCVMTFYBEGKEVITNIEIRVAGITTEPI-EVITIS 253
 Qy 248 PNDHVVYKEKGEELLPCTVYFSPFLMDSRNEVMTIDGKKPDITIDVT-----INESI 302
 Db 254 PLETTI--PASLSRLIYPCVFLGTGSSNTIYWM-----MANSTISVAVPRGRVTEGL 306
 Qy 303 SHSRTE-DETRIOI-LSIKKVTSEDLKRSYVJARSAKGVAAKVKQKVPAPRYTEL 360
 Db 307 HHQYSNDEYVAVSLIFDVTKEIDLNTDFKCVATNPRSPQSILHTYKE-----VSS 358
 Qy 361 ACGFATVLLVLLIYVHYVYL 363
 Db 359 TFSMGIALAPLSLILVGAIMI 381

RESULT 9

Fit-1M protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jan-2000

C:Accession: S42633

R:Berger, G.; Reikertorfer, A.; Braselmann, S.; Gruninger, P.; Busslinger, M.

EMBO J. 13, 1176-1188, 1994

A:Title: Alternative promoter usage of the Fos-responsive gene Fit-1 generates mRNA isoforms

A:Reference number: S42632; PMID:94178260; PMID:8131748

A:Accession: S42633

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-247 <BER>

C:Superfamily: Interleukin-1 receptor type I

Query Match

7.0%; Score 256; DB 2; Length 247;

Best Local Similarity 30.8%; Pred. No. 8e-12;

Matches 70; Conservative 45; Mismatches 80; Indels 32; Gaps 9;

Qy 346 KVKQVAP-RYVTEALCGFATVLLVILVYVHYVLEMLFYRAHFGDTEILDKGE 404
 Db 2 RLRKQPIDHOSITYIVAGSLLMFLINVLIVLTKFIMVALFMDIMAPYKTONDKL 61
 Qy 405 YDIYVSAR-----NMEEEFVLLTLRGVLENEGYQACIFDRSDSGNTEAVFD 456
 Db 62 YDAIYIIPVFRSAGATGSVEFYVHYTLPOVLENGCYGLQYGRDLFGQDAATVES 121
 Qy 457 FIDSRMIVLSP-----DYTEKISMLEPKAGMCONSTATKIVYERPL-EHPH 509
 Db 122 SIGNSRQVFLVLPNMMHSKEFAYEQEIAL--HSALQNN--SKVITLMEPMGEASR 175
 Qy 510 PGILQKESVSF-----VSWKGE--KSKHS-GSKFVKALRLALPL 546
 Db 176 LQGLDQDSLQHLVKMGQTTIKMRDHVADKQSLSSKFWKVRVYQMPV 222

RESULT 10

interleukin-1 receptor type II - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S17428

R:McMahon, C.J.; Slack, J.L.; Mosley, B.; Cosman, D.; Lupton, S.D.; Brunton, L.L.; C

EMBO J. 10, 2821-2832, 1991

A:Title: A novel IL-1 receptor, cloned from B cells by mammalian expression, is expt

A:Reference number: S17428; PMID:92007725; PMID:1833184

A:Accession: S17428

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-398 <MCMA>

A:Cross-references: EMBL:X59770; NID:G33796; PIDN:CAA42441.1; PID:G33797

C:Keywords: cytokine receptor; transmembrane protein

Query Match

6.9%; Score 252; DB 2; Length 398;

Best Local Similarity 23.4%; Pred. No. 3.2e-11;

Matches 79; Conservative 51; Mismatches 148; Indels 60; Gaps 13;

Qy 20 ASERCDDWGLDTRQIOVEDEPARIKCPLEFHEFLKFNSTAHSAGLTLIWTRODRDL 79
 Db 24 AARSCFRGRHRYKBEFL-EGEPVALRCQPVWYMAVSPP-----INLTHKNDASRTV 78
 Qy 80 --EELNFRLENRISKEKDVLMFRPTLNDTGNATYCMLENTTYSKVAFLPEVQKDS 137
 Db 79 PGRE-----ETRWMAQGALMLPALQEDSGTYVCTTRNASYCDKMSIELVFEVNTDA 131
 Qy 138 FNSPMKLPHVHKYIEV-----GIQRTCPNVDGYFPSSVKKPTITWMCYKIQNFN 188
 Db 132 F-----LP-----FISYPQILTLSTSGV--LVCPDSEFTRDKTDVKIQWKSLLDKDN 180
 Qy 189 NVIPBGMNLSPLI--ALISNNNGYTCVATYBENGRTFHLTELTLYKVVGPSKNAVPIV 245
 Db 181 EKFLSVRGTHLLVHDVLEADGYRCVLTFAHEGQYVITISIELRIKKKEETI-PVI 239
 Qy 246 HSPNDHVVYKEKGEELLPCTVYFSPFLMDSRNEVMTIDGKKPDITIDVTINESISHS 305
 Db 240 ISPLKTI--SASIGSRLTIPCKVFLGTGTPPLTLMMLWTAN-----DTHIESAVPG 288
 Qy 306 RTEDERTIOI-----LSIKKVTSEDLKRSYVJARSAKGVAAKVKQKVPAPRYTEL 360
 Db 289 RYLEGPRQYSENENYIEVPLIFDVTREDLAMDQFC 326

RESULT 11

ST2 protein - human

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C:Accession: S30444

R:Tomimaga, S.; Yokota, T.; Yanggiawa, K.; Tsukamoto, T.; Takagi, T.; Tetsuka, T.

Biochim. Biophys. Acta 1171, 215-218, 1992

A: Variety: strain Ankara
 C: Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
 C: Accession: T37450
 R: Antoinette, G.; Scheffinger, F.; Falkner, F.G.; Dörner, F.
 Submitted to the EMBL Data Library, March 1997
 A: Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
 A: Reference number: Z20877
 A: Accession: T37450
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-326 <AMT>
 A: Cross-references: EMBL:U94848; PIDN: AAB96555.1
 A: Experimental source: strain Ankara
 C: Genetics:
 A: Note: MVA184R
 C: Superfamily: vaccinia virus B1SR protein; immunoglobulin homology

Very Match: 5.2%; Score 189; DB 2; Length 326;
 est Local Similarity 25.1%; Pred. No. 1.4e-06;
 Matches 84; Conservative 57; Mismatches 154; Indels 40; Gaps 18;

QY 8 VSIIYF-GIIQSDASECDWGLDMRQIOVPEDEPARICPLFEHFLKNTSTASAGL 66
 DB 9 LSIFFYSSPVQTNAPPCIDKG-QYFASFMELNEPVLPCPOI-NLISGYNL-----L 61
 QY 67 TLITWTRQDRLDEPINFRLPENRISKEKDVLMFRPTLNDGNYTQMLNNTYCSKVA 126
 DB 62 DILMEKRGADNDRIIFID-----NGSNMLIANPT-OSDSGIYICITTNETICDMMKS 111
 QY 127 FPLFVQKDSCFNSPMKLPHKLYIEYGIORITCPNVDSVPSSVKPTITWYMGCKYION 186
 DB 112 LNTIYVSNSNIDLISYF-QIVNERSIGBMVCPNINAFASVNDIIT-SGHRLR- 167
 QY 187 FNNVIEGKMLSLIALISNN-GNITCVVTPYENGRTFHLTRLTVKVGSPRAVPPV 244
 DB 168 -MRLQRTFGITIEIVRKNDAGYVCLEYIGKTYVTRIIVKLEV---RDKLIIPST 223
 QY 245 IHSPPNDHVVYKEKEGELLICTYVPSFLMDSRN-EVWMTIDK-KPDITIDVTINES 301
 DB 224 MQLPEGVVT---SIGSNLTACRV--SLRPTTDADVFMSNGYVEEDDGDGGRISVA 278
 QY 302 IHSRTEDETR--TOILSIKKVTSIDLKRSYVCHA 334
 DB 279 NKIYMT-DKRRVITSRLNINPVKEED-ATFTCTMA 311

SULT 15
 T20992
 hypothetical protein F15G9.4a - Caenorhabditis elegans
 C: Species: Caenorhabditis elegans
 C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C: Accession: T20992; T24733
 R: Sulston, J.
 Submitted to the EMBL Data Library, December 1994
 A: Reference number: Z19355
 A: Accession: T20992
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-5175 <ML>
 A: Cross-references: EMBL:Z47068; PIDN: CAA87335.1; GSPDB: GN00028; CESP: F15G9.4a
 A: Experimental source: clone F15G9
 R: Kerehaw, J.
 Submitted to the EMBL Data Library, December 1994
 A: Reference number: Z19929
 A: Accession: T24733
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-5175 <ML>
 A: Cross-references: EMBL:Z47070; PIDN: CAA87344.1; GSPDB: GN00028; CESP: F15G9.4a
 A: Experimental source: clone T0989
 C: Genetics:
 A: Gene: CESP: F15G9.4a
 A: Map position: X

A: Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 118
 ; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 30
 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5

Query Match: 5.2%; Score 189; DB 2; Length 5175;
 Best Local Similarity 21.6%; Pred. No. 7.3e-05;
 Matches 141; Conservative 87; Mismatches 227; Indels 198; Gaps 39;

QY 72 WTRQDRLDEPINFRLPENRISKEKDVLMFRPTLNDGNYTQMLNNTYCSKVA 131
 DB 3515 WREGDK---PV-YLYDRYSISPDGSHITINAKSLSDGKTYICRASNEAGTSDIDLILKI 3569
 QY 132 ----VQKDSCFNSPMKLPHKLYIEYGIORITCPNVDSVPSSVKPTITWYMGCKYI-Q 185
 DB 3570 LVPEKIDKNNIIGNPLAIYARTIYLE-----CP-ISGI-----PQPDVIWTKNGMDINN 3617
 QY 186 FNNVIEGKMLSLIALISNN-GNITCVVTPYENGRTFHLTRLTVKVGSPK---NA 240
 DB 3618 TDSRVILAQNNETFGIENQVTDGGRYTCTAT-NRGGKASH---DPSLDVLSPPEDIDHG 3673
 QY 241 VPPVTHSPNDHVVYKEKEGELLICTYVPSFLMDSRN-EVWMTIDK-KPDITIDVTIN 229
 DB 3674 TQPTI-----KREDDTTTLCTPIGLAEDIDAOVMDVSWTKSRLLDG---DLTON 3720
 QY 300 ESISHRTEDETRTOILSIKKVTSIDLKRSYVCHASAKGEVAKAKVQKVP----- 352
 DB 3721 VDIS-----DQGRKLTISQASLEMGU---YTCIALNRAGEASLEKVEILSPVIDISR 3772
 QY 353 ---APRYVE---LACGEGATVLLVILIVYH---VYMLEMVLFPYRAHFGTDETIID 401
 DB 3773 NDVQPVAVANQPTIRKCA-----VGHPPPSIKMLK-----N 3804
 QY 402 GKRYDIYVSYARNAR-EEFVILITRGVLENEFGYKLCIFPDSILPGANTYAVAPDIO 459
 DB 3805 GKE---VTDDENIRLVEGOVYQILIR-TDSHAGKMSCVARND--GVKELEMYVD--- 3854
 QY 460 RSRMTIVLSPPYVTEKS---ISMLEFKGMCONSIATKLVIVRYRPLEHPHPILOK 516
 DB 3855 -----VTFPVVYSKSNPIKALGETITLFCNMS-----GNPVP---QLK 3891
 QY 517 ---ESVSFVSWKGEKSKHSGKFWKALALP-LRSLASAS---SGMNSCSGSDISL 567
 DB 3892 WAKGSLIFDSDPDGARISLKA-----RLDIPHLKKTQVGVYTCQALNAGTSSEASGV 3945
 QY 568 DHVQRRSRRLKEPPELOSSERAAGSPAPAGKMSKIRGSSATRCCTVYTCBGENHLRMS 627
 DB 3946 D-----VLVPEPI-NRDGIDMSFRLP-----AQSSTLQOC---LAQG----- 3978
 QY 628 RABINHPQWETHLCKPVPOBSETQIONGTRELPAPPOISALALHFTDLSN 680
 DB 3979 -----KPVPO---MRTTLNGTALTLTSTPGITVASDSSTFIQINN 4013

Search completed: April 23, 2003, 08:54:58
 Job time : 56 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:44:25 ; Search time 27 Seconds
(without alignments)

1055.342 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669
Sequence: 1 MTLMLCVSLYFYGLQSDA.....SALALHFTDLSNNNDFFYL 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	493.5	13.5	ILIR_RAT	002955 ratius norv
2	484.5	13.2	ILIR_MOUSE	P13504 mus musculu
3	424.5	11.6	ILIR_HUMAN	P14738 homo sapien
4	314	8.6	ILIS_MOUSE	P27931 mus musculu
5	302	8.2	ILIS_RAT	P43303 ratius norv
6	261	7.1	ILIS_CERAT	Q29612 ceropithec
7	252	6.9	ILIS_HUMAN	P27930 homo sapien
8	230.5	6.3	IRLI_MOUSE	P14719 mus musculu
9	229.5	6.3	IRLI_HUMAN	Q01838 homo sapien
10	189	5.2	VB16_VACCV	P25122 vaccinia vl
11	187	5.1	VB16_COMPX	Q04523 compox viru
12	182	5.0	VB16_VACCC	P21116 vaccinia vl
13	174	4.7	TLR1_MOUSE	Q99P41 mus musculu
14	164	4.5	TLR2_HUMAN	Q06003 homo sapien
15	163.5	4.5	TLR6_MOUSE	Q99C99 mus musculu
16	161.5	4.4	TLR6_MOUSE	Q99C99 mus musculu
17	159	4.3	TLR2_CHICK	P08953 drosophila
18	154.5	4.2	TLR2_CHICK	Q99C96 gallus gall
19	153	4.2	TLR2_MACFA	Q95553 macaca fasc
20	151.5	4.1	MY88_MOUSE	P22366 mus musculu
21	148.5	4.0	CAML_MOUSE	P11627 mus musculu
22	147.5	4.0	TLR1_HUMAN	P15399 homo sapien
23	147	4.0	TLR7_MOUSE	P58681 mus musculu
24	145	4.0	TLR2_BOVIN	Q951A9 bos tauris
25	143.5	3.9	TLR4_HUMAN	Q00206 homo sapien
26	142.5	3.9	TLR4_PAPAN	Q9TSP2 papio anubi
27	142.5	3.9	TLR4_PAPAN	Q9TSP2 papio anubi
28	141.5	3.9	TLR4_BOVIN	Q9G165 bos tauris
29	139	3.8	MY88_HUMAN	Q99336 homo sapien
30	138	3.8	TLR2_MOUSE	Q99K17 mus musculu
31	138	3.8	TLR2_MOUSE	Q99K17 mus musculu
32	136.5	3.7	TL21_CHICK	Q94D78 gallus gall
33	136	3.7	KMLS_CHICK	P11799 gallus gall

34	135.5	3.7	1257	1	CAML_HUMAN	P32004 homo sapien
35	134	3.7	1284	1	NRCA_CHICK	P35331 gallus gall
36	133	3.6	1333	1	VGRI_MOUSE	P35969 mus musculu
37	133	3.6	2012	1	DSCA_HUMAN	O60469 homo sapien
38	132	3.6	784	1	TLR2_CRIGR	Q91168 cricetus
39	131.5	3.6	1259	1	CAML_RAT	O05695 ratius norv
40	130	3.5	1049	1	TLR7_HUMAN	O99YK1 homo sapien
41	129.5	3.5	819	1	FGRI_CHICK	P21804 gallus gall
42	129	3.5	808	1	FGRI_MOUSE	Q03142 mus musculu
43	129	3.5	822	1	FGRI_RAT	O04589 ratius norv
44	128	3.5	822	1	FGRI_HUMAN	P13362 homo sapien
45	127.5	3.5	823	1	CRK3_CHICK	P18461 gallus gall

ALIGNMENTS

RESULT 1	ID	ILIR_RAT	STANDARD:	PRT:	576 AA.
AC	002955;				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Interleukin-1 receptor, type I precursor (IL-1R-1) (P80).				
GN	ILIR1 OR IL1RA.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_Taxid=10116;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Ganglion;				
RX	MEDLINE=9326794; PubMed=7684399;				
RA	Hart R.P., Liu C., Shadick A.M., McCormack R.J., Jonakait G.M.;				
RT	"An mRNA homologous to interleukin-1 receptor type I is expressed in				
RL	cultured rat sympathetic ganglia.";				
J. Neuroimmunol. 44:49-56(1993).					
CC	- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),				
CC	AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO				
CC	THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.				
CC	- SIMILARITY: CONTAINS 1 TIR DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	-----				
DR	EMBL; M95578; AAA16196.1; ALT_SEQ.				
DR	HSSP; P14778; IL1RA.				
DR	InterPro: IPR004076; ILIR_receptor.				
DR	InterPro: IPR004075; IL1_receptor1.				
DR	InterPro: IPR004074; IL1_receptor1/IL1.				
DR	InterPro: IPR003006; IG_MHC.				
DR	InterPro: IPR003600; IG_1like.				
DR	InterPro: IPR000157; TIR_domain.				
DR	Pfam; PF00047; ig; 2.				
DR	Pfam; PF01582; TIR; 1.				
DR	PRINTS; PRO1538; INTRLEUKINR1.				
DR	PRINTS; PRO1536; INTRLEUKINR12F.				
DR	PRINTS; PRO1537; INTRLEUKINR1F.				
DR	SMART; SM00410; IG_1like; 1.				
DR	SMART; SM00255; TIR; 1.				
DR	PROSITE; PS50104; TIR; 1.				
KW	Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;				
KW	Repeat; Phosphorylation.				
FT	SIGNAL	1	19		BY SIMILARITY.
FT	CHAIN	20	576		INTERLEUKIN-1 RECEPTOR, TYPE I.

```

FT DOMAIN 20 338 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 339 359 POTENTIAL.
FT DOMAIN 360 576 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 113 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 138 206 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 244 322 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 386 544 TIR.
FT DISULFID 25 107 BY SIMILARITY.
FT DISULFID 46 99 BY SIMILARITY.
FT DISULFID 145 199 BY SIMILARITY.
FT DISULFID 251 315 BY SIMILARITY.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD RES 556 556 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 576 AA; 66758 MW; 55B20C92385A34A CRC64;

Query Match 13.5%; Score 493.5; DB 1; Length 576;
Best Local Similarity 26.5%; Pred. No. 7.6e-30;
Matches 153; Conservative 105; Mismatches 230; Indels 89; Gaps 25;

47 CPLEFHLKFNYSSTAHSAGLTLVWYTRDRLDEEPINFLPENRISKEKQVLMFRPFTL 106
46 CPLTPNEMH-----GGTIIVY-----KNDSTPIASD-KDSRIHQONHLMFVPAKM 91

OY 107 NDTGNVYTMRLNTYCSKVAAPLEVOKDS--CFNSPMKLVHKLVEYGIQRTCPND 164
OY 92 EDGGYCYCIMNSTYCKTKITMSVLENDPCLCYNTQASF-IQRLHVA-GDGSIVCEYLD 149
OY 165 GYF--PSSVVFITVWNGCKIKQNFNNVIBGMALSFILALISNN-----GNTTCVY 216
OY 150 -FPEDDENNELPKQWYKNCPLP-----LDDGNFGRKNKLMVNAVEHRGANTYCRISY 203
OY 217 PENCRTFHLTRTLTVKVGSPKNAVPVHSPNDVYVEKEGELLIPCTVYFSFLMDS 276
OY 204 TYGCKQVPTVITVITITIDSKRP-REVINSFRBETM-EDAPGSTIQLICNVTOF---- 257
OY 277 RNEVWMTIDGKPD-DITIDVTINESISH-SRTEDETRTOILSIKYSEDLKRSYVCHA 334
OY 258 TDLYVWKMNGSEIEMDDPILAEYQFLEHPSAKKRYTLITLTVNSEVKSQFYRYPFCV 317
OY 335 RSAGKGVAAKAKYKQKPARPYTWELACGRATLVILVIVHYVWLENVLYRYAHFG 394
OY 318 KNT--HILETAHVLVYVPDPFNKYLIGGFALTATVAFCAICYKVFVDIVLWYRSCS 375
OY 395 --TDETLLDGKEYDIYVSANAE-----EEFVLLTLRGVLENERGYKLCIFDRDLP 446
OY 376 DFLPRKASDGRITVAVLYLKYTGEGSAVYDTPFKLPEVLGQFGYKFLICGRDYY 435
OY 447 GGNTEAVFDEFIQSRMIVVLSPDYVTEKSIIMLEFK-LGWMCONSIA-----TK 496
OY 436 GEDTIEVTNENVKSRRLIILVVD-----MGSEFCLOOSEBQIAIYDALIREGIK 487
OY 497 LIVVEYRPLHPHPCIIQKESVSFVS-----WKG---EKSAGSGKFKKALRLPL 546
OY 488 IILELEKIOEYR---KMPESIOFIKQKGAICWSDGFKRPSAKTRFWKNLRYOMPA 543
OY 547 RSLASAGSGMNESSQSOSDILDHVORRRSRLEKPEL 583
OY 544 QRS-----PLSKGHLLITLDPVLDTEKYLQAEHL 573

RESULT 2
ILIR MOUSE STANDARD; PRT; 576 AA.
ID ILIR MOUSE
AC P13504;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor, type I precursor (IL-1R-1) (P80).
GN ILIR1 OR ILIRA OR IL-IR1.

```

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-45.
RX MEDLINE=88290679; PubMed=2969618;
RA Sims J.B., March C.J., Cosman D., Widmer M.B., McDonald H.R.,
RA McMahon C.J., Grubin C.B., Wiggall J.M., Jackson J.L., Call S.M.,
RA Friend D., Alpert A.R., Gillis S., Urdal D.L., Dower S.K.;
RT "cDNA expression cloning of the IL-1 receptor, a member of the
RT immunoglobulin superfamily."
RL Science 241:585-589(1988).
RN [2]
RP PHOSPHORYLATION OF THR-556.
RX MEDLINE=91254338; PubMed=1828344;
RA Bird T.A., Woodward A., Jackson J.L., Dower S.K., Sims J.B.;
RT "Phorbol ester induces phosphorylation of the 80 kilodalton murine
RT interleukin 1 receptor at a single threonine residue."
RL Biochem. Biophys. Res. Commun. 177:61-67(1991).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B)
CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO
CC THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC -----
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CC -----
OY 217 PENCRTFHLTRTLTVKVGSPKNAVPVHSPNDVYVEKEGELLIPCTVYFSFLMDS 276
OY 204 TYGCKQVPTVITVITITIDSKRP-REVINSFRBETM-EDAPGSTIQLICNVTOF---- 257
OY 277 RNEVWMTIDGKPD-DITIDVTINESISH-SRTEDETRTOILSIKYSEDLKRSYVCHA 334
OY 258 TDLYVWKMNGSEIEMDDPILAEYQFLEHPSAKKRYTLITLTVNSEVKSQFYRYPFCV 317
OY 335 RSAGKGVAAKAKYKQKPARPYTWELACGRATLVILVIVHYVWLENVLYRYAHFG 394
OY 318 KNT--HILETAHVLVYVPDPFNKYLIGGFALTATVAFCAICYKVFVDIVLWYRSCS 375
OY 395 --TDETLLDGKEYDIYVSANAE-----EEFVLLTLRGVLENERGYKLCIFDRDLP 446
OY 376 DFLPRKASDGRITVAVLYLKYTGEGSAVYDTPFKLPEVLGQFGYKFLICGRDYY 435
OY 447 GGNTEAVFDEFIQSRMIVVLSPDYVTEKSIIMLEFK-LGWMCONSIA-----TK 496
OY 436 GEDTIEVTNENVKSRRLIILVVD-----MGSEFCLOOSEBQIAIYDALIREGIK 487
OY 497 LIVVEYRPLHPHPCIIQKESVSFVS-----WKG---EKSAGSGKFKKALRLPL 546
OY 488 IILELEKIOEYR---KMPESIOFIKQKGAICWSDGFKRPSAKTRFWKNLRYOMPA 543
OY 547 RSLASAGSGMNESSQSOSDILDHVORRRSRLEKPEL 583
OY 544 QRS-----PLSKGHLLITLDPVLDTEKYLQAEHL 573

FT CHAIN 20 576 INTERLEUKIN-1 RECEPTOR, TYPE I.
FT DOMAIN 20 338 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 339 359 POTENTIAL.
FT DOMAIN 360 576 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 113 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 138 206 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 244 322 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 386 544 TIR.
FT DISULFID 25 107 BY SIMILARITY.
FT DISULFID 46 99 BY SIMILARITY.
FT DISULFID 145 199 BY SIMILARITY.
FT DISULFID 251 315 BY SIMILARITY.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD RES 556 556 PHOSPHORYLATION (BY PKC).
 SQ SEQUENCE 576 AA; 66697 MW; 7AA8304C86412A16 CRC64;
 Query Match 13.2%; Score 484.5; DB 1; Length 576;
 Best Local Similarity 25.8%; Nred. No. 3,7e-29;
 Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;
 QY 34 QIOFEDDEPARI-----KCPLEHFLKFNSTASHASAGLTLIWTRODRLE 81
 DB 21 EIDCTYPMQIVLFLSVNEIDIRKCPLEPKM-----GDTIIMY-----KNDST 67
 QY 82 PINRLPENRISKEKDVLMFEPRLTNDTGNLTCLAMNTYCSKVAFLPVOKDS--CFN 139
 DB 68 PISAD RDSRIHOONEHLMFPAVEDSGTYICLVNSTYTLKTKVTYVLENDPGLCYG 126
 DB 140 SPMLPVHKLIEYGIORTCPNDGYF--PSSVKEPTITWYMGCKI0NFNNV1PEGMT 197
 DB 127 TOATFP-ORLHIA-GDGLVCPYV-SYFKDENNELPEVQYKNC-KPILLDNVSGVVD 182
 QY 198 SPFLALIS--NNGNYTCVATYTPENGRTFLTRITLVKVGSPKAVPVVHSPMDHYVE 255
 DB 183 KLIVRNAVAEHRGDYICRMSTYFRGKQYPTVVIQPTIDENKRD-RPVILSPENETI-E 240
 QY 256 KEPGEELLICTVYFSLDMSRNEWMTIDGKPDITIDVTINES-----ISHRT 307
 DB 241 ADPSMQLICNTVGF-----SDLVYKKNMS-----ELEMWDPLAEDYQVEHPST 289
 QY 308 EDE-TRTQILSIKKVTSEDLKRSVYCHASAGKAVAKVOKVAPARYVELACGFGA 366
 DB 290 KRKYTLITLTINISVKSQFRYPFCVAKNT--NIFSAHQVLYPVPDFENYVIGFII 347
 QY 367 TVLLVLIIVHYVYEMVLFYPAHAG--TDEITLDGEKDYIVSYARNAE-----E 418
 DB 348 LRTATVCCVCIYKFKVDIVLWYDSCSGFLPSKASGKTYDAVILPKTLGEGSFSDDL 407
 QY 419 EPLLTLRGVLENGVYKLCIFPDSDLPAGNTVAVDFIORSRMIVLSPD----- 471
 DB 408 TFFPKLPVLEGGFGKLTLYGDDYVGGDTLEVTNENKSKRLTILVRDGGFSWL 467
 QY 472 -VYTEKSIIMLEFPLGVMCONSIATKLIIVEYRPLE--HHPGIIQ-LKESVSVKSG- 526
 DB 468 GQSEEGIAL-----YNNLIQEGI--KIVLLELEKIDQYKMPDSIQIKKHGIVICMSGD 521
 DB 527 --EKSKSGSKFKALRLALPLNSLSASSGMSGSCSQSDISLDHVRRSRL 577
 DB 522 FOERPOSAKTRFWKMLFYOMPAGRS-----PLSKRLLTLDPVADTEKL 567
 RESULT 3
 ILIR HUMAN STANDARD; PRT; 569 AA.
 ID ILIR HUMAN
 AC P14778;
 DT 01-APR-1990 (Rel. 14, Last Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-1 receptor, type I precursor (IL-1R-1) (IL-1R-alpha)
 DE (P80) (Antigen CD121a).
 GN ILIR1 OR ILIRA OR ILIR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90098789; PubMed=2533321;
 RA Chua A.O., Gubler U.;
 RT "Sequence of the cDNA for the human fibroblast type interleukin-1
 receptor.";
 RL Nucleic Acids Res. 17:10114-10114(1989).
 RN (2)

RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=90046906; PubMed=2530587;
 RA Sims J.E., Acres R.B., Grubin C.E., McMahon C.J., Wignall J.M.,
 RA March C.J., Dower S.K.;
 RT "Cloning the Interleukin 1 receptor from human T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8946-8950(1989).
 RN (3)
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 18-332 IN COMPLEX WITH IL1B.
 RX MEDLINE=97215903; PubMed=9062193;
 RA Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J.;
 RT "Crystal structure of the type-1 interleukin-1 receptor complexed
 with interleukin-1beta.";
 RL Nature 386:190-194(1997).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 21-331 IN COMPLEX WITH IL1RA.
 RX MEDLINE=97215904; PubMed=9062194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
 RA Sarubbi E., Akesson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "A new cytokine-receptor binding mode revealed by the crystal
 structure of the IL-1 receptor with an antagonist.";
 RL Nature 386:194-200(1997).
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
 CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO
 CC THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD121a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd121a.htm".
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X16896; CAA34773.1; -
 CC EMBL; M27492; AAB59137.1; -
 DR PIR; S06928; S06928.
 DR PIR; A36187; A36187.
 DR PDB; 1IRB; 04-PEB-98.
 DR PDB; 1IRA; 17-JUN-98.
 DR Genew; HGNC:5993; ILIR1.
 DR MIM; 147810; -
 DR InterPro; IPR004076; ILIR_receptor.
 DR InterPro; IPR004075; IL1_receptor1.
 DR InterPro; IPR004074; IL1_receptor1/1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR000157; TIR_domain.
 DR Pfam; PF00047; Ig_2.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO1538; INTERLEUKIN1.
 DR PRINTS; PRO1536; INTERLEUKIN1F.
 DR PRINTS; PRO1537; INTERLEUKIN1F.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PSS0104; TIR; 1.
 KW Immunoglobulin domain; Transmembrane; Glycoprotein; Receptor; Signal;
 KW Repeat; 3d-structure.
 FT SIGNAL 1 17
 FT CHAIN 18 569 INTERLEUKIN-1 RECEPTOR, TYPE 1.
 FT DOMAIN 18 336 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 337 356 POTENTIAL.
 FT DOMAIN 357 569 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 37 103 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 135 203 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 241 319 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 383 541 TIR.
 FT DISULFID 23 104

QY 365 GATVLLVILVYHYVWLEMLFYRAHGTDTILDGKEYDI 407
DB 368 ---PLSLIILVV---GAIMRRRCRRA-----GKTYGL 395

RESULT 5
ILIS_RAT STANDARD; PRT; 416 AA.

ID ILIS_RAT
AC P43303;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor, type II precursor (IL-1R-2).
GN IL1R2 OR IL1RB OR IL-1R2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;

SEQUENCE FROM N.A.
RX MEDLINE=95035882; PubMed=7524717;
RA Bristol J. Gatti S., Malinowsky D., Bjork L., Sundgren A.K.,
RA Bartal T.;
RT "Interleukin-1 stimulates the expression of type I and type II
RT interleukin-1 receptors in the rat insulinoma cell line R1msf;
RT sequencing a rat type II interleukin-1 receptor cDNA.";
RL Eur. Cytokine Netw. 5:319-330(1994).
CC - FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC or send an email to license@isb-sib.ch).

DR EMBL, Z22812; CAA80465.1; -
DR InterPro; IPR004074; IL1_receptor/IL1.
DR InterPro; IPR004077; IL1_receptor/IL1.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
PFam: PF00047; ig_3.
PRINTS; PRO1539; INTERLEUKIN2.
PRINTS; PRO1536; INTERLEUKIN12F.
DR SMART; SM00409; IG_3.
KW Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
KW Repeat.
FT SIGNAL 1 13 POTENTIAL.
FT CHAIN 14 416 INTERLEUKIN-1 RECEPTOR, TYPE II.
FT DOMAIN 14 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 381 POTENTIAL.
FT DOMAIN 382 416 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 57 127 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 157 226 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 263 345 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFID 64 120 BY SIMILARITY.
FT DISULFID 164 219 BY SIMILARITY.
FT DISULFID 270 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 46353 MW; 50EFBA4881C5D4E CRC64;
SQ SEQUENCE 416 AA; 46353 MW; 50EFBA4881C5D4E CRC64;

Query Match 8 2% Score 302; DB 1; Length 416;
Best Local Similarity 25.3%; Pred. No. 1,7e-15;
Matches 97; Conservative 67; Mismatches 153; Indels 66; Gaps 18;
QY 25 DDW--GLDTRQIOVEDPARIKCPLFEHFLKFNSTASHAGLTLIWTWRQDRLEEP 82

DB 41 DCWFRGRDRKSELR.L-EGEPVILRCPLVPH-----SDTSSSSRSL-L-TWSKSDSOLLP 92
QY 83 INFRLEPNRISKQVIAWRLPILNDTGNVTCMLNNTYCSKAPAFLELVQDSCFNPM 142
DB 93 GD---EPRMWWKDDTLWVLPVAVQDGGTYICTFRNASHCEQWSELEKVFK-----NTBA 143
QY 143 KLPVHKLYIEYGIQRT---CPNVDGPPSSVSKPTTYWMCYKIQNNVNYPEGNNLS 198
DB 144 SFLVVS-VIQISALSTGLVCPDLKEFISRTDQKIQYK-----SILLDGNNK 194
QY 199 FLIA-----LISNN-----GNVTCVTVYENGRKTHLTRLTKVYSPKNAVPIVHS 247
DB 195 FLGADPTRLILSNITSMGADGYRCVMTFTYEKENVITRNIELRVKGIITTEPI-FVILS 253
QY 248 PNDHVYKEPEBEILLPTCVTFPSFLMDSRNVMWMTIDKKDDITDVT-----INESI 302
DB 254 PLETT--PASLSRLVPCVKFLGTSTNTYVW-----MANSTFISVAYPRGRYTEGL 306
QY 303 SHSRTE-DETRTQI--LSIKVTSBDLKRSYVCHASAKGEVAAKVKQVPAPRYVEL 360
DB 307 HHOYSNDENVYEVSLIPPTVKEDLNDTRKCVATNPRFQSLHTTVE-----VSS 358
QY 361 ACQFGATVLLVILVYHYVWL 383
DB 359 TSWGIALAPSLIILVGAIMI 381

RESULT 6
ILIS_CERAB STANDARD; PRT; 393 AA.

ID ILIS_CERAB
AC Q29612;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor, type II precursor (IL-1R-2) (IL-1R-beta).
GN IL1R2 OR IL1RB.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
CC [1]
CC SEQUENCE FROM N.A., AND SEQUENCE OF 125-145.
RX MEDLINE=96355446; PubMed=8702856.
RA Liu C., Hart R.P., Liu X.J., Clevenger W., Maki R.A., Souza E.B.;
RT "Cloning and characterization of an alternatively processed human
RT type II interleukin-1 receptor mRNA.";
RL J. Biol. Chem. 271:20965-20972(1996).
CC - FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA
CC (IL-1B), AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
CC - SUBCELLULAR LOCATION: THE LONG ISOFORM IS A TYPE I MEMBRANE
CC PROTEIN WHILE THE SHORT ISOFORM IS SOLUBLE.
CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.
CC - SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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DR EMBL, U64092; AAB05876.1; -
DR EMBL, U64093; AAB05877.1; -
DR HSSP; P14778; IIRB.
DR InterPro; IPR004074; IL1_receptor/IL1.
DR InterPro; IPR004077; IL1_receptor/IL1.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003600; IG_Like.

Pfam: PF00047; ig: 3.
 DR PRINTS; PRO1539; INTERLEUKINR2.
 DR PRINTS; PRO1536; INTRLEUKINR2P.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00410; IG; 1.
 DR Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
 KW Repeat; Alternative splicing.
 FT SIGNAL 1 13
 FT CHAIN 14 393
 FT DOMAIN 14 347
 FT TRANSMEM 348 368
 FT DOMAIN 369 393
 FT DOMAIN 43 115
 FT DOMAIN 145 214
 FT DOMAIN 251 333
 FT DISULFID 50 108
 FT DISULFID 152 207
 FT CARBOHYD 258 326
 FT CARBOHYD 66 66
 FT CARBOHYD 72 72
 FT CARBOHYD 112 112
 FT CARBOHYD 219 219
 FT CARBOHYD 277 277
 FT VARSPLIC 297 393
 SQ SEQUENCE 393 AA; 44778 MW; D4D746C5DE569A8 CRC64;
 Query Match 7.1%; Score 261; DB 1; Length 393;
 Best Local Similarity 21.9%; Pred. No. 2, 1e-12;
 Matches 89; Conservative 64; Mismatches 185; Indels 68; Gaps 15;
 QY 20 ASERCDWGLDTRQIOVFEDEPARIKCPLEHFKLNSTANASAGLTLYMTROQRDL 79
 DB 24 AASCVPRGHYKKEEFL-EGEPVALKCPQ---VPQLAASVPHNLTHKNDASAMV 78
 QY 80 --SEPIFRLEPERISKEKDLVFRPTLADTGYTCMLNTTYCSKVAPELVQKQSC 137
 DB 79 PGEE-----ETRMNQDGLMILPALQDSGYICTTNASACDVSLELNFEE----- 127
 QY 138 FNSPMKLPVHKLTYEY-----GIQRTCPNVDSYPPSSVAKPTITWYGCYKIQNFN 188
 DB 128 -NTDASLP-----FISYPOILTLSTFGV--LVCPDLREFTRDKTGKIQWYKDFLPDKDN 180
 QY 189 NVFPEGNNLSFLI---ALISNNNGYTVVYPPENGRTFHLTRTLTVKVVSPKNAVPEVI 245
 DB 181 EKPLSVAGTTHLVADVALDAGYRCVLFAHEGQOYNITRNLTEILKKEEETI--PVI 239
 QY 246 HSPNDHVVYEKEPEEELLICTVYVFSFLMSRNEVMWTIDCKKPPDYITIDVTINESISHS 305
 DB 240 ISPLKTI--SASLGSRLTTPCKVFLGTGTPLTLMWMTAN-----DTHVESATPGG 288
 QY 306 RTEDETRTQI-----LSIKVYTSBDLKRSYVCHASAKGEVAKAKVYKQKVPAP 354
 DB 289 RVEGPRQSESENNENYIEVPLIFDPTRKDLNNVFCFYNWTFGOTLRFTTVE--PPP 346
 QY 355 RYTYELACGEGATLVLLVYVHVYVMEVLFYRAHFGDETLI 400
 DB 347 TFS-----WGIVLAPLALFVLVGIWMHRRCKHRTGKADGLTVL 386
 RESULT 7
 IL1S_HUMAN STANDARD; PRT; 398 AA.
 AC P27930; Q9UB68;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-1 receptor, type II precursor (IL-1R-2) (IL-1R-beta)
 DE (UniProt Cbm121b).
 GN IL1R2 OR IL1RB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxId=9606;
 FT

RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE=92007725; PubMed=1833184;
 RA McMahon C.J., Slack J.L., Mosley B., Cosman D., Lupton S.D.,
 RA Brunton L.L., Grubin C.E., Wignall J.M., Jenkins N.A., Brannan C.I.,
 RA Copeland N.G., Huebner K., Croce C.M., Cammizzaro L.A., Benjamin D.,
 RA Dower S.K., Spriggs M.K., Sime J.E.;
 RT "A novel IL-1 receptor, cloned from B cells by mammalian expression,
 RT is expressed in many cell types.";
 RL EMBO J. 10:2821-2832 (1991).
 [2]
 RP SEQUENCE FROM N.A.
 RA Chou H.-H., Takashiba T., Takigawa M., Maeda H., Asahara Y.,
 RA Nishimura F., Arai H., Murayama Y.;
 RT "Complete nucleotide sequence and expression of the human
 RT interleukin-1 receptor type II in human gingival fibroblasts.";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA Mead K., Maupin R., Yoakum M., Hottel M.;
 RT "The sequence of Homo sapiens BAC clone RP11-451C2.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
 CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTRAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CDM121b entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdm121b.htm".
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 CC -----
 DR EMBL; X59770; CAA42441.1; -;
 DR EMBL; U74649; AAD00242.1; -;
 DR EMBL; AC007165; AAK52072.1; -;
 DR PIR; S17428; S17428.
 DR HSP; P14778; IITB.
 DR Genew; HGNC:5994; IL1R2.
 DR MIM; 147811; -;
 DR InterPro; IPR004074; IL1_receptor/II.
 DR InterPro; IPR004077; IL1_receptor/II.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; ig; 3.
 DR PRINTS; PRO1539; INTERLEUKINR2.
 DR PRINTS; PRO1536; INTRLEUKINR2P.
 DR SMART; SM00409; IG; 3.
 DR Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
 KW Repeat.
 FT SIGNAL 1 13
 FT CHAIN 14 398
 FT DOMAIN 14 343
 FT TRANSMEM 344 369
 FT DOMAIN 370 398
 FT DOMAIN 43 115
 FT DOMAIN 145 214
 FT DOMAIN 251 333
 FT DISULFID 50 108
 FT DISULFID 152 207
 FT DISULFID 258 326
 FT CARBOHYD 66 66
 FT CARBOHYD 72 72
 FT CARBOHYD 112 112
 FT CARBOHYD 219 219
 FT CARBOHYD 277 277
 FT CONFLICT 123 123
 FT CONFLICT 171 171
 FT
 POTENTIAL.
 INTERLEUKIN-1 RECEPTOR, TYPE II.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 IG-LIKE C2-TYPE DOMAIN 1.
 IG-LIKE C2-TYPE DOMAIN 2.
 IG-LIKE C2-TYPE DOMAIN 3.
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 L-> F (IN REF. 2).
 K-> R (IN REF. 2).

FT	CONFLICT	199	199	L -> 0 (IN REF. 2)
50	SEQUENCE	398 AA,	45421 MM,	2C2A03ADAEF3AC5B CR664;
	Query Match		6.9%;	Score 252; DB 1; Length 398;
	Best Local Similarity		23.4%;	Pred. No. 1e-11;
	Matches 79;	Conservative	51;	Mismatches 148; Indels 60; Gaps 13
QY	20	ASERCDWGLDMTRQIQVEDEPARIKCPFEHFLKFNSTASHAGLTILWTRODRDL	79	
DB	24	AARSQRFRRGRHYKREFR-L-EGEFVALRCQVPMWMAVSPPR----	INLTWHRKDSARFY 78	
QY	80	--EKPINFLPENRISKEDVLMFRFTLINDGNNTYCMRLNTYGSKVAAPPELVQKDCS	137	
DB	79	PCSE-----ETRWMAQDQALMLPALQBDSSCTTYCTTRNASYCDKMSIELEVFENTDA	131	
QY	138	FNSPMKL PVHKLVIIEY-----GIORITCVNVDGYPSSVKPTITWYMGCKIQNFN	188	
	132	F-----LP-----FISVPQILTLTSTGV--LVGCDLSEFPRDKTDVNIQWYKOSLIDKDN	180	
QY	189	NVIPRCANLSFLI--ALISNNGNTYTCVVTYPENGRFTFLTRTLTKVVGSPKNAVPPVI	245	
DB	181	EKFLSVRGCTHLLVMDVALDADGYACVCLTFPAHQGOYNTIRSIHRIRKKKEETI-PVI	239	
QY	246	HSPNDHVVYKRPGEELLPCVTYFSEFLMDSNRHWMTIDGKKPDDITIDVTINISHS	305	
DB	240	ISPLKTI--SASIGSLRLLPCRFVFLGTGTPPLTTMLMTAN-----DTHIESAVPGG	288	
QY	306	RTEDERTQI-----LSIKVTSDDLKRSYVC	332	
DB	289	RYTEGPRQREYSNNENYIEVPLIFDPTVTRFDLLMDPKC	326	
	RESULT 8			
	IRLL MOUSE			
ID	IRLL MOUSE	STANDARD;	PRT;	337 AA.
AC	PI4719;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin 1 receptor-like 1 precursor (ST2 protein) (TL protein)			
DN	(Lymphocyte antigen 84).			
GN	IL1RL1 OR ST2 OR ST2 OR LY84.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
CC	NCBI_TaxId=10090;			
	[1]			
KE	SEQUENCE FROM N.A.			
RC	STRAIN=BAIB/c;			
RA	MEDLINE=90092495; PubMed=2532153;			
RA	Tomliana S.;			
RT	"A putative protein of a growth specific cDNA from BAIB/c-3T3 cells			
RT	is highly similar to the extracellular portion of mouse interleukin 1			
RL	receptor."			
RL	FEBS Lett. 258:301-304(1989).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=C3H/He; TRISUB=SpLeen;			
RA	MEDLINE=91355215; PubMed=1832015;			
RA	Tomliana S. I.; Jenkins N.A.; Gilbert D.J.; Copeland N.G.;			
RA	Tetsuka T.;			
RT	"Molecular cloning of the murine ST2 gene. Characterization and			
RT	chromosomal mapping."			
RL	Biochim. Biophys. Acta 1090:1-8(1991).			
RN	[3]			
RN	SEQUENCE FROM N.A.			
RC	MEDLINE=89345536; PubMed=2527364;			
RA	Klemenz R.; Hoffmann S.; Werenkiold A.K.;			
RT	"Serum- and oncoprotein-mediated induction of a gene with sequence			
RT	similarity to the gene encoding carcinoembryonic antigen."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:5708-5712(1989).			
CC	-1- FUNCTION: POSSIBLY INVOLVED IN REGULATION OF T-LYMPHOCYTE			
CC	ACTION.			

DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR004078; Interlnl_BP.
 DR Pfam: PF00047; Ig; 3.
 DR PRINTS; PRO1540; INTRLEUKN1BP.
 DR PRINTS; PRO1536; INTRLEUKN12P.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00410; Ig_Like; 1.
 DR Immunoglobulin domain; Glycoprotein; Repeat; Signal.
 KW SIGNAL.
 FT CHAIN 1 18
 FT INTERLEUKIN-1 BINDING PROTEIN.
 FT DOMAIN 1 326
 FT DOMAIN 2 135
 FT DOMAIN 3 235
 FT DISULFID 48
 FT DISULFID 143
 FT DISULFID 194
 FT DISULFID 242
 FT CARBOHYD 80
 FT CARBOHYD 103
 FT CARBOHYD 113
 FT CARBOHYD 206
 FT CARBOHYD 237
 SQ SEQUENCE 326 AA; 36593 MW; 7F03F64600BE390 CRC64;

Query Match 5.2%; Score 189; DB 1; Length 326;
 Best Local Similarity 24.0%; Pred. No. 4.8e-07;
 Matches 80; Conservative 60; Mismatches 156; Indels 38; Gaps 16;

QY 8 VSIFY-GLI0SDASERCDMDGLTMRQIOVFEDPARIKCPLEHFLKPNYSTAHSAGL 66
 DB 9 LSIFFSSFVQTFNAPBCIDKG-QYFASFMELNEPVLPEQI-NLTSSGYNL-----L 61
 QY 67 TLIVWTRORDLEEPINFLPENRISKEDVLMFRPLNDTGNVTCMLNNTTYSKVA 126
 DB 62 DIMERKRGANDRIIPID-----NGSNMLINPT-QSDSGIYICITNRTYCDMMS 111
 QY 127 FPLEVQKDCSPNPKLPHKLYIEYGIORITCPNVGSPSVKPTITWMCYKION 186
 DB 112 LNTIYVSNSNDLISYP-QIYNERSTGBMVCENINAFASVANADIIW-SGHRIR- 167
 QY 187 FNNVIEPGMNLSPILALISNN-GNYTCVVTYPENGRFTLRLTVKVGSPKNAVPPV 244
 DB 168 -NRKQRTGKITIEVRKNDAGVTCVLEYIGKTYNTRIVKLEV--RKLIIPST 223
 QY 245 HSPNDHVYKEBGEELIPCTYFSEFLMDSRN-EYWMITDGKKPDITITVINESIS 303
 DB 224 MQLPDGIIVT---SIGSNLITACRV--SLRPPTDADVFWMISNGMYEEDDGDGRISVA 278
 QY 304 HSRTEDETR---TQILSIKKVTSSEDLKRSVCHA 334
 DB 279 NKIYTDKRRVITSRLININPKED-ATFTTCMA 311

RESULT 11
 VB16 COMPLEX STANDARD; PRT; 326 AA.
 ID VB16 COMPLEX
 AC 004523;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-1 binding protein precursor (Protein B16).
 GN B16R OR B15R.
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_Taxid:10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brighton red;
 RA MEDLINE=93008237; PubMed=1339315;
 RA Spriggs M.K., Hruby D.E., Maliszewski C.R., Pickup D.J.,
 RA Sims J.E., Buller R.M.L., Vanslyke J.;

RT "Vaccinia and cowpox viruses encode a novel secreted interleukin-1-
 RT binding protein.";
 RL Cell 114:145-152(1992).
 CC -!- FUNCTION: BINDS INTERLEUKIN-1 AND POSSIBLY INTERLEUKIN-6. COULD
 CC PREVENT THESE CYTOKINES REACHING THEIR NATURAL RECEPTORS. IN
 CC CONSEQUENCE THE INFLAMMATORY RESPONSE WOULD BE DIMINISHED AND
 CC VIRUS REPLICATION ENHANCED.
 CC -!- SUBCELLULAR LOCATION: VIRION, CELL SURFACE OR SECRETORY
 CC GLYCOPROTEIN.
 CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -!- SIMILARITY: STRONG, TO INTERLEUKIN-1 RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; M95202; AA85776.1; -
 DR InterPro: IPR004074; IL1_receptor/IL1.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR004078; Interlnl_BP.
 DR Pfam: PF00047; Ig; 3.
 DR PRINTS; PRO1540; INTRLEUKN1BP.
 DR PRINTS; PRO1536; INTRLEUKN12P.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00410; Ig_Like; 1.
 KW Immunoglobulin domain; Glycoprotein; Repeat; Signal; Early protein.
 FT SIGNAL 1 18
 FT INTERLEUKIN-1 BINDING PROTEIN.
 FT DOMAIN 1 326
 FT DOMAIN 2 135
 FT DOMAIN 3 235
 FT DISULFID 48
 FT DISULFID 143
 FT DISULFID 194
 FT DISULFID 242
 FT CARBOHYD 80
 FT CARBOHYD 103
 FT CARBOHYD 113
 FT CARBOHYD 237
 SQ SEQUENCE 326 AA; 36790 MW; 7AE2064A1FPAF54 CRC64;

Query Match 5.1%; Score 187; DB 1; Length 326;
 Best Local Similarity 25.4%; Pred. No. 6.8e-07;
 Matches 85; Conservative 60; Mismatches 147; Indels 42; Gaps 19;

QY 10 LYRY-GLI0SDASERCDMDGLTMRQIOVFEDPARIKCPLEHFLKPNYSTAHSAGLT 68
 DB 11 IFFYSSFVQTFNAPBCIDKG-QYFASFMELNEPVLPEQI-NLTSSGYNLID 63
 QY 69 IMWTRORDLEEPINFLPENRISKEDVLMFRPLNDTGNVTCMLNNTTYSKVAEP 128
 DB 64 DIMERKRGANDRIIPID-----NGSNMLINPT-QSDSGIYICITNRTYCDMMSLN 113
 QY 129 LEVQKDCSPNPKLPHKLYIEYGIORITCPNVGSPSVKPTITWMCYKION- 186
 DB 114 LTVI---SVSESNIDISYQIYNERSTGBMVCENINAFASVANADIIW-SGHRIRNK 169
 QY 187 -FNNVIEPGMNLSPILALISNNGNYTCVVTYPENGRFTLRLTVKVGSPKNAVPPV 245
 DB 170 RLQRPFGITITIDVNR-NDAGYTCVLYTGDTYVTVTRIVKLEV--RDRMLPTM 224
 QY 246 HSPNDHVYKEBGEELIPCTYFSEFLMDSRN-EYWMITDGK-KPDITITVINESI 302
 DB 225 QLP-DGVV--TSIGSNLITACRV--SLRPPTDADVFWMISNGMYEEDDGDGRISVA 278
 QY 303 HSRTEDETR---TQILSIKKVTSSEDLKRSVCHA 334
 DB 279 NKIYTDKRRVITSRLKINPKED-ATFTTCMA 311

RESULT 12

ID	VB16_VACC	STANDARD;	PRT;	326 AA.
AC	P21116;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-1 binding protein precursor (Protein B16).			
GN	B16.			
OS	Vaccinia virus (strain Copenhagen).			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Orthopoxvirus.			
OX	NCBI_TaxID=10249;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=91021027; PubMed=2219722;			
RA	Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,			
RA	Paolletti E.;			
RT	"The complete DNA sequence of vaccinia virus.";			
RT	Virology 179:247-266(1990).			
CC	[2]			
CC	COMPLETE GENOME.			
CC	Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,			
CC	Paolletti E.;			
CC	"Appendix to 'The complete DNA sequence of vaccinia virus.'";			
CC	Virology 179:517-563(1990).			
CC	-1- FUNCTION: BINDS INTERLEUKIN-1 AND POSSIBLY INTERLEUKIN-6. COULD			
CC	PREVENT THESE CYTOKINES REACHING THEIR NATURAL RECEPTORS. IN			
CC	CONSEQUENCE THE INFLAMMATORY RESPONSE WOULD BE DIMINISHED AND			
CC	VIRUS REPLICATION ENHANCED			
CC	-1- SUBCELLULAR LOCATION: VIRION, CELL SURFACE OR SECRETORY			
CC	GLYCOPROTEIN.			
CC	-1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	-1- SIMILARITY: STRONG, TO INTERLEUKIN-1 RECEPTORS.			
CC	-1- CAUTION: This is a conceptual translation; a stop codon was			
CC	readover in position 31.			
CC	-----			
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CC	-----			
DR	EMBL; M35027; AAA48214.1; ALT_SEQ.			
DR	PIR; P42527; P42527.			
DR	InterPro: IPR003599; IG.			
DR	InterPro: IPR003006; IG_MHC.			
DR	InterPro: IPR003600; IG_1like.			
DR	Pfam; PF00047; IG; 3.			
DR	SMART; SMO0409; IG; 3.			
DR	SMART; SMO0410; IG_1like; 3.			
KM	Immunoglobulin domain; Glycoprotein; Repeat; Signal.			
FT	SIGNAL	1	18	POTENTIAL.
FT	CHAIN	19	326	INTERLEUKIN-1 BINDING PROTEIN.
FT	DOMAIN	41	106	IG-LIKE C2-TYPE DOMAIN 1.
FT	DOMAIN	135	201	IG-LIKE C2-TYPE DOMAIN 2.
FT	DOMAIN	235	316	IG-LIKE C2-TYPE DOMAIN 3.
FT	DISUFID	48	99	BY SIMILARITY.
FT	DISUFID	143	194	BY SIMILARITY.
FT	DISUFID	242	309	BY SIMILARITY.
FT	CARBOHYD	80	80	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	103	103	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	206	206	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	237	237	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	326 AA;	36661 MW;	A064B534EBCB64BF CR64;

Query Match 5.0%; Score 182; DB 1; Length 326;

Best Local Similarity 24.9%; Pred. No. 1.6e-06;

Matches 83; Conservative 56; Mismatches 154; Indels 40; Gaps 18;

RESULT 13

ID	TLR1_MOUSE	STANDARD;	PRT;	795 AA.
AC	Q9EP01; Q9EP05;			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Toll1-like receptor 1 precursor (Toll1/interleukin-1 receptor-like)			
DE	(TIR).			
GN	TLR1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	STRAIN-BALB/C; TISSUE=Macrophage;			
RA	MEDLINE=20558581; PubMed=11095740;			
RA	Ozinsky A., Underhill D.M., Fontenot J.D., Hajjar A.M., Smith K.D.,			
RA	Wilson C.B., Schroeder L., Aderem A.;			
RT	"The repertoire for pattern recognition of pathogens by the innate			
RT	immune system is defined by cooperation between Toll1-like			
RT	receptors.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 97:13766-13771(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	TISSUE=Macrophage;			
RA	MEDLINE=20571875; PubMed=11123271;			
RA	Hajjar A.M., O'Mahony D.S., Ozinsky A., Underhill D.M., Aderem A.,			
RA	Kiebanoff S.J., Wilson C.B.;			
RT	"Functional interactions between Toll1-like receptor (TLR) 2 and TLR1			
RT	or TLR6 in response to phenol-soluble modulin.";			
RN	J. Immunol. 166:15-19(2001).			
RP	[3]			
RA	SEQUENCE FROM N.A.			
RA	STRAIN-BALB/C; TISSUE=Spleen;			
RA	Thomson D.P., Campbell C.C., Liew F.Y., Xu D.;			
RT	"Cloning of Mus musculus Toll1-like receptor 1.";			
RT	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Participates in the innate immune response to microbial			
CC	agents. Cooperates with TLR2 and modulates the response to			
CC	microbial constituents. Acts via MyD88 and TRAF6, leading to NF-			
CC	kappa-B activation, cytokine secretion and the inflammatory			
CC	response (by similarity).			
CC	-1- SUBUNIT: Binds TLR2 via their respective extracellular domains.			
CC	Binds MyD88 via their respective TIR domains (by similarity).			

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
 CC phagosomes.
 CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN
 CC -1- SIMILARITY: CONTAINS 9 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 DR EMBL: AY009154; AAC37302.1; -
 DR EMBL: AF316985; AAC35062.1; -
 DR HSSP: 060603; 1FTW.
 DR MGD: MGI:1341295; TIR1.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_Tyr.
 DR InterPro: IPR00157; TIR_domain.
 DR Pfam: PF00560; LRR_8.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01582; TIR_1.
 DR PRINTS: PRO0019; LEURICRPT.
 DR SMART: SM00370; LRR_3.
 DR SMART: SM00082; LRRCT_1.
 DR SMART: SM00369; LRR_Typ_6.
 DR SMART: SM00255; TIR_1.
 DR PROSITE: PS50104; TIR_1.
 DR Receptor; Immune response; Inflammatory response; Signal;
 DR Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
 KM TIR SIGNAL 1 25
 FT CHAIN 26 795
 FT DOMAIN 26 582
 FT TRANSMEM 583 603
 FT DOMAIN 604 795
 FT REPEAT 46 70
 FT REPEAT 71 94
 FT REPEAT 96 116
 FT REPEAT 117 140
 FT REPEAT 174 197
 FT REPEAT 200 223
 FT REPEAT 247 270
 FT REPEAT 296 319
 FT REPEAT 333 356
 FT CARBOHYD 432 432
 FT CONFLICT 88
 SQ SEQUENCE 795 AA; 90672 MW; 855356429872D232 CRC64;
 Query Match 4.7%; Score 174; DB 1; Length 795;
 Best Local Similarity 20.2%; Pred. No. 2.3e-05;
 Matches 117; Conservative 95; Mismatches 200; Indels 166; Gaps 26;
 QY 98 VLMFPP-----TLNDNTNYTCMLNTTYCSKVAFLFVVGQDSCFNPMLKLPVHKLYI 151
 DB 270 IYWHIPVVKFISNVTGQOGLAFKRMNYSYDTISKALSHQVTD-VFSPPQSY-ITSIFA 327
 QY 152 EYGIQRTCPN---VDGYPSSVVKPTI-----TWYGCYKI 184
 DB 328 NNNTIGFTWSTGTHMVHMLCPSSQVSPFLAVDPTDNLTLTDVWFKDCRNLVRLKTLISLQKNQL 387

QY 185 QNFNNVIEGKMLSPFLIAL-INSNGNYTCVTPYPPNGRTFHLTRITLV-----KYVSP 237
 DB 388 KNLNENIILTSAMKTSLOKLDISONS-----LRYSDGIPICANTOSILVNLSSNMLTGSV 442
 QY 238 KNAVPP-----VHSNDHNVYEKRGDEL-----LIPTVYFSLMDR 277
 DB 443 FRCPLPKVKVLDLHNNRIMSIPKD--VYHQLQELNVAASNLTDLPGGARSS----- 494
 QY 278 NNVWMTIDOKKRDQDTIDVTINESISHRTED-----ETRTQI 315
 DB 495 -----ISVLVIDNSVSHR-SEDFQSCQINRSLTAGNPPQCTCELRDVR 539
 QY 316 LSIKVTSEDLK---RSYVC-HARSAKGEVAKAKVKKVPAPRYTVELACFGATVLLV 371
 DB 540 KNIGVAREVVGWPDSTRCDVPSSRGTAIDPHMS---PLSCDTVLLVTIGATMLVL 596
 QY 372 VI---LIVVHVHVMENLVF-----YRAHGTDETLIDKGEYDIYVSYARNAEEERY 421
 DB 597 AVTGAFLCLYFDLPVYVRLCMQOTRHRARHIPIELQRLNQLQFAPVSY--SGHDSAVV 654
 QY 422 LITLGVLENERGYLCLIFDRDPLPGNTEAVPFIQSRREMIYVLSPDYVT----- 474
 DB 655 KNEILPNLEKD-DIQICLHERNFVPEKSTVENIINTEKSYKSTIFVLSHPFIQSEKCHYE 713
 QY 475 -----EKSIEMLEPKLGVMCONSIATKLIYERYPLEHPHGGILQLKESVSVSM 524
 DB 714 LYFAHNLHFEHSDMLILALPIQYSIPT-----NHKKLK-----TWSRRYTLWM 761
 QY 525 KEEKSHSGSKPKWKALRLALPLRSLSASSGWNSSCSQ 562
 DB 762 PTEKNKH--GLFWANILRASINVKLVNQAE--TCYTO 794
 RESULT 14
 TLR2 HUMAN STANDARD; PRT; 784 AA.
 AC 060603; 015454;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Toll-like receptor 2 precursor (Toll/interleukin 1 receptor-like protein 4).
 GN TLR2 OR TIL4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte, and Prostate;
 RX MEDLINE=98261424; PubMed=959645;
 RA Chaudhary P.M., Ferguson C., Nguyen V., Nguyen O., Maesa H.F., Eby M.,
 RA Jasmin A., Trask B.J., Hood L., Nelson P.S.;
 RT "Cloning and characterization of two Toll/interleukin-1 receptor-like
 RT genes TIL3 and TIL4: evidence for a multi-gene receptor family in
 RT humans";
 RL Blood 91:4020-4027 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98118556; PubMed=9435236;
 RA Rock F.L., Hardiman G., Timans J.C., Kastlein R.A., Bazan J.F.,
 RT "A family of human receptors structurally related to Drosophila
 RT Toll";
 RN Proc. Natl. Acad. Sci. U.S.A. 95:588-593 (1998).
 RN [3]
 RP SEQUENCE FROM N.A., AND RESPONSE TO LIPOPOLYSACCHARIDE.
 RC TISSUE=Fetal lung;
 RX MEDLINE=98421677; PubMed=9751057;
 RA Yang R.-B., Mark W.R., Gray A., Huang A., Xie M.H., Zhang M.,
 RA Goddard A., Wood W.I., Gurney A.L., Godowski P.J.;
 RT "Toll-like receptor-2 mediates lipopolysaccharide-induced cellular
 RT signaling";
 RL Nature 395:264-268 (1998).

GN TLR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=placenta;
RX MEDLINE=99250250; PubMed=10231569;
RA Takeuchi O., Kawai T., Santo H., Copeland N.G., Gilbert D.J.,
Jenkins N.A., Takeda K., Akira S.,
"TLR6: A novel member of an expanding Toll-like receptor family.";
Gene 231:59-65(1999).
[2]
RN (1)
RP MEDLINE=21334385; PubMed=11441107;
RX Bulut Y., Faure E., Thomas V., Equils O., Arditi M.,
"Cooperation of Toll-like receptor 2 and 6 for cellular activation by
soluble tuberculosis factor and Bordetella burgdorferi outer surface
protein A lipoprotein: role of Toll-interacting protein and Il-1
receptor signaling molecules in Toll-like receptor 2 signaling.";
J. Immunol. 167:987-994(2001).
CC -1- FUNCTION: Participates in the innate immune response to Gram-
positive bacteria and fungi. Acts via MyD88 and IRAF6, leading to
NF-kappa-B activation, cytokine secretion and the inflammatory
response. Recognizes mycoplasma macrophage-activating
lipopeptide-2KD (MALP-2), soluble tuberculosis factor (STF),
phenol-soluble modulin (PSM) and B.burgdorferi outer surface
protein A lipoprotein (Ospa-L) cooperatively with TLR2.
CC -1- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
phagosomes (by similarity).
CC -1- TISSUE SPECIFICITY: Detected in monocytes, CD11c+ immature
dendritic cells, plasmacytoid pre-dendritic cells and dermal
microvessel endothelial cells.
CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC -1- SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
DR EMBL; AB020807; BAA78631.1; -
DR HSSP; O60603; 1FTW. TLR6.
DR Genew; HGNC:16711; TLR6.
DR MIM; 605403; -
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00370; LRR; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
DR Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 31
FT CHAIN 32 796 TOLL-LIKE RECEPTOR 6.
FT DOMAIN 32 586 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 587 607 POTENTIAL.
FT DOMAIN 608 796 CYTOPLASMIC (POTENTIAL).
FT REPEAT 51 74 LRR 1.
FT REPEAT 75 98 LRR 2.

FT REPEAT 100 120 LRR 3.
FT REPEAT 121 144 LRR 4.
FT REPEAT 158 175 LRR 5.
FT REPEAT 176 201 LRR 6.
FT REPEAT 222 248 LRR 7.
FT REPEAT 276 302 LRR 8.
FT REPEAT 302 328 LRR 9.
FT REPEAT 340 366 LRR 10.
FT REPEAT 366 392 LRR 11.
FT REPEAT 392 418 LRR 12.
FT REPEAT 418 444 LRR 13.
FT DOMAIN 444 784 TIR.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 583 583 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 796 AA; 91889 MW; 35CEAEC05BFA8BD CRC64;

Query Match 4.5%; Score 163.5; DB 1; Length 796;
Best Local Similarity 20.3%; Pred. No. 0.00015;
Matches 118; Conservative 91; Mismatches 192; Indels 179; Gaps 26;

QY 103 PTLNDTGN-----YTCHLR-----NTTYSKV-----APF 128
DB 249 PTLNFTLNHLETTWKCIIVRQPLMPREVETLNTYNTLIESIIEEDFTYSKTLKALT 308
QY 129 LEVQKDSQFNPMKLPYHKLVIEXGIQRI-----CPNDGYFPSSVK----- 172
DB 309 IHHITNOVFLPSQTL--YTFSENNIMTLTISDTPPIHMLCPHA--PSTFKELNFTQ 362
QY 173 --PTTWGTCYKIONFNVNI--PEGNNISPLIALIS-----NNGANYTC 212
DB 363 NVFTSIEFKSTLYKLETLILQKNGLDLFGVGLMTQDMSLEILDVSNLSGSRHKS 422
QY 213 VVTYENGRTFLNRTLLTVKVGSPKAAVPPY-----HSPNDHYVKEKPEEELLIPCT 267
DB 423 NCTWVESIVLNLSSNM--LTDVFRCLPPRIKYLIDHSNKIKSVPOVVLEALQELN 479
QY 268 VYFSLMDSRNEMVMTIDG--KKPDITIDVTINESISHRTE----- 308
DB 480 VAFNSLTD-----LPCGGSFSSLSVLIIDHNSVSHPSADPFOSCOQMSIKKGDNF 531
QY 309 ---DEFTQILSIKKVTSIDLK--RSYVC--HARSAGEVAAKAKVKOPAPRYTVELA 361
DB 532 OCTCLAREFVNKIDQVSSEVLBGWDSYKCDYPSYRSPLKDFMS-----ELS 581
QY 362 CG-----FGATVLLVILIVVHY-----WLEMLVLY-----RAHGTDETLIDGKE 404
DB 582 CNIITLIVIGATMVLAVTVSLCLIVLDPYLLMVCQMTQTRRARANIIPLEEQRIHQ 641
QY 405 YDIYVSYARNAREEFVLLTLAGVLENFQYKLCIFDSDSLPGCVTVAVPFIQSRBM 464
DB 642 FFAFTISYSEH--DSAMVSELVPIYLEKE--DIQICLHEENPFGKSIIVENITINICKSYKS 698
QY 465 IVLSPDYVT-----EKSISMLEPKLGVMCONSITATGLIVVEYRPLEH 507
DB 699 IVLSPNFVQSWCHYELFPAHNLPHGSSNNLILILEPIPNQSIPIPK-----YHKLK- 752
QY 508 PHRGILQKESVSPVSKGKSGKSHSGKFKWALRALPLR 547
DB 753 -----ALMTQGTYLQMPKESKR--GLFWANIRAAFPNMK 784

Search completed: April 23, 2003, 08:52:18
Job time : 32 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:45:00 ; Search time 95 Seconds

(without alignments)
1490.046 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MRLMCVSLYFYGIQSDA.....SALALHFTDLNNNDFFIL 687

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_21.*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2586	70.5	570	4	014915
2	2327.5	63.4	570	11	061730
3	2313.5	63.1	570	11	063621
4	1892	51.6	356	4	09NPH3
5	1663	45.3	360	11	08VCB9
6	825	22.5	686	4	09NPH6
7	817.5	22.0	658	4	09NPH6
8	806.5	22.0	686	11	09ERS6
9	769.5	21.0	696	4	09NPH3
10	767.5	20.9	696	4	09NPH3
11	528	14.4	541	4	013478
12	496	13.5	555	13	090874
13	479	13.1	537	11	061098
14	477.5	13.0	567	6	005208
15	471.5	12.9	599	4	095256
16	471.5	12.9	599	4	095256

17	470	12.8	566	11	062611	062611 ractus norv
18	466	12.7	574	11	09ERS7	09ERS7 mus musculu
19	463.5	12.6	556	4	09UQ44	09UQ44 homo sapien
20	457.5	12.5	533	13	09DER5	09DER5 gallus gall
21	457.5	12.5	533	13	09DER1	09DER1 gallus gall
22	457	12.5	561	11	062929	062929 ractus norv
23	446	12.2	614	11	0922B1	0922B1 mus musculu
24	445.5	12.1	575	4	09HB29	09HB29 homo sapien
25	444.5	12.1	562	4	013525	013525 homo sapien
26	428.5	11.7	354	11	09ER66	09ER66 mus musculu
27	390	10.6	486	13	09DER4	09DER4 gallus gall
28	390	10.6	486	13	09DER2	09DER2 gallus gall
29	347.5	9.5	571	13	08QFN4	08QFN4 salmo salar
30	258	7.0	280	11	062692	062692 ractus norv
31	239.5	6.5	403	6	09N2H5	09N2H5 equus cabal
32	228	6.2	321	13	09DER6	09DER6 gallus gall
33	228	6.2	321	13	09DER3	09DER3 gallus gall
34	222.5	6.1	410	4	09H733	09H733 homo sapien
35	220	6.0	336	11	062612	062612 ractus norv
36	214	5.8	409	11	09JLZ8	09JLZ8 mus musculu
37	196.5	5.4	1356	5	08WRE2	08WRE2 anopheles g
38	192.5	5.2	795	5	09NPK8	09NPK8 drosophila
39	192.5	5.2	795	5	09XZF9	09XZF9 drosophila
40	192.5	5.2	795	5	09VJX9	09VJX9 drosophila
41	190	5.2	326	12	08V4R4	08V4R4 monkeypox v
42	189.5	5.2	1152	5	08WRE5	08WRE5 anopheles g
43	189	5.2	326	12	057261	057261 vaccinia vi
44	189	5.2	5198	5	076518	076518 caenorhabd
45	188	5.1	441	13	09DDC4	09DDC4 oncorhynch

ALIGNMENTS

RESULT 1
ID 014915 PRELIMINARY; PRT; 570 AA.
AC 014915;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE IL-1 receptor accessory protein (Membrane interleukin 1 receptor accessory protein).
GN IL1RAP.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Huang J., Gao X., Li S., Cao Z.;
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Saio T., Seki N.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE OF 118-179 FROM N.A.
RC MEDLINE=98140136; PubMed=9479509;
RA Dale M., Hammond D.W., Cox A., Nicklin M.J.H.;
RL "The human gene encoding the interleukin-1 receptor accessory protein (IL1RAP) maps to chromosome 3q28 by fluorescence in situ hybridization and radiation hybrid mapping."
RN (4)
RP SEQUENCE FROM N.A.
RC MEDLINE=20261666; PubMed=10799889;
RA Jensen L.B., Muzio M., Mantovani A., Whitehead A.S.;
RL "IL-1 signaling cascade in liver cells and the involvement of a soluble form of the IL-1 receptor accessory protein."
J. Immunol. 164:5277-5286(2000).

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DR EMBL; AF029213; AAB84059.1; -
DR EMBL; AB006537; BAA25421.1; -
DR EMBL; AF016261; AAC39609.1; -
DR EMBL; AF167342; AAF71689.1; -
DR EMBL; AF167335; AAF71689.1; JOINED.
DR EMBL; AF167336; AAF71689.1; JOINED.
DR EMBL; AF167337; AAF71689.1; JOINED.
DR EMBL; AF167338; AAF71689.1; JOINED.
DR EMBL; AF167339; AAF71689.1; JOINED.
DR EMBL; AF167340; AAF71689.1; JOINED.
DR EMBL; AF167341; AAF71689.1; JOINED.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00047; IG_2.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTRLNRI1F.
DR SMART; SM00409; IG; 2.
DR SMART; SM00255; TIR; 1.
KW Receptor.
SQ SEQUENCE 570 AA; 65418 MW; 5F47F8DDECA98B8A CRC64;

Query Match 70.5%; Score 2586; DB 4; Length 570;
Best Local Similarity 85.3%; Pred. No. 5.8e-211;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

QY 1 MTLIMCVSLVYFGIILQSDASERCDDWGLDTRQIQVEDEPARIKCPLEHFLKFNYST 60
DB 1 MTLIMCVSLVYFGIILQSDASERCDDWGLDTRQIQVEDEPARIKCPLEHFLKFNYST 60
QY 61 AHSAGLTLLIWMYTRQDRDLPEEPINFRLENRISKEKDVLMFRPTLNDTGYTCMLRNTT 120
DB 61 AHSAGLTLLIWMYTRQDRDLPEEPINFRLENRISKEKDVLMFRPTLNDTGYTCMLRNTT 120
QY 121 YCSKVAPELEVQKDSCEPNSPMKLPVHKLIEYGIQRTCPNDGYPSSVKPTITVMYG 180
DB 121 YCSKVAPELEVQKDSCEPNSPMKLPVHKLIEYGIQRTCPNDGYPSSVKPTITVMYG 180
QY 181 CYKIQNFNNVPIPEGNNLSFLLIALISNNNGNTCVVTPYENGRTFHLTRTLTVKVGSPKNA 240
DB 181 CYKIQNFNNVPIPEGNNLSFLLIALISNNNGNTCVVTPYENGRTFHLTRTLTVKVGSPKNA 240
QY 241 VPPVISHPNDDVYVEKEGEEELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
DB 241 VPPVISHPNDDVYVEKEGEEELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
QY 361 ACFGATVLLVLLIVVHYVWLEMLVFRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
DB 361 ACFGATVLLVLLIVVHYVWLEMLVFRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
QY 421 VLLTRGVLENEFGYKLCIFDRDSLPGNTVEAVPFIQSRMIVVLSPPYTEKISIM 480
DB 421 VLLTRGVLENEFGYKLCIFDRDSLPGNTVEAVPFIQSRMIVVLSPPYTEKISIM 480
QY 481 LEFLGVMCNSIATK---LIVVEYRPLEBHPHGLQLES---VSFVSMKGEKSHSG 533
DB 481 LEFLGVMCNSIATK---LIVVEYRPLEBHPHGLQLES---VSFVSMKGEKSHSG 533
QY 534 SKFWKALRLALPLRSLSSAGSNESCSSOSDI 565
DB 534 SKFWKALRLALPLRSLSSAGSNESCSSOSDI 565
QY 536 GFWKQLOVAMPVKKSPRRSSSDEQGLSYSSL 567
DB 536 GFWKQLOVAMPVKKSPRRSSSDEQGLSYSSL 567

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DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DB Interleukin 1 receptor accessory protein precursor.
GN IL1RAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95293970; PubMed=775431;
RA Gelfand S.A., Nunes P., Kwee L., Labow M., Chizzonite R.A., Ju G.;
RT "Molecular cloning and characterization of a second subunit of the
RT Interleukin 1 receptor complex.";
RT J. Biol. Chem. 270:13757-13765(1995).
DR EMBL; X85999; CAAS9991.1; -.
DR MGI; MGI:104975; Il1rap.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00047; IG; 3.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTRLNRI1F.
DR SMART; SM00409; IG; 2.
DR SMART; SM00255; TIR; 1.
KW Receptor; Signal.
FT SIGNAL 1 20
SQ SEQUENCE 570 AA; 65740 MW; 4D4B07E0310AFDC5 CRC64;

Query Match 63.4%; Score 2327.5; DB 11; Length 570;
Best Local Similarity 75.9%; Pred. No. 5.3e-189;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

QY 1 MTLIMCVSLVYFGIILQSDASERCDDWGLDTRQIQVEDEPARIKCPLEHFLKFNYST 60
DB 1 MGLIMVLSLSFGIILQSHASERCDDWGLDTRQIQVEDEPARIKCPLEHFLKFNYST 60
QY 61 AHSAGLTLLIWMYTRQDRDLPEEPINFRLENRISKEKDVLMFRPTLNDTGYTCMLRNTT 120
DB 61 AHSAGLTLLIWMYTRQDRDLPEEPINFRLENRISKEKDVLMFRPTLNDTGYTCMLRNTT 120
QY 121 YCSKVAPELEVQKDSCEPNSPMKLPVHKLIEYGIQRTCPNDGYPSSVKPTITVMYG 180
DB 121 YCSKVAPELEVQKDSCEPNSPMKLPVHKLIEYGIQRTCPNDGYPSSVKPTITVMYG 180
QY 181 CYKIQNFNNVPIPEGNNLSFLLIALISNNNGNTCVVTPYENGRTFHLTRTLTVKVGSPKNA 240
DB 181 CYKIQNFNNVPIPEGNNLSFLLIALISNNNGNTCVVTPYENGRTFHLTRTLTVKVGSPKNA 240
QY 241 VPPVISHPNDDVYVEKEGEEELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
DB 241 VPPVISHPNDDVYVEKEGEEELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
QY 361 ACFGATVLLVLLIVVHYVWLEMLVFRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
DB 361 ACFGATVLLVLLIVVHYVWLEMLVFRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
QY 421 VLLTRGVLENEFGYKLCIFDRDSLPGNTVEAVPFIQSRMIVVLSPPYTEKISIM 480
DB 421 VLLTRGVLENEFGYKLCIFDRDSLPGNTVEAVPFIQSRMIVVLSPPYTEKISIM 480
QY 481 LEFLGVMCNSIATK---LIVVEYRPLEBHPHGLQLES---VSFVSMKGEKSHSG 533
DB 481 LEFLGVMCNSIATK---LIVVEYRPLEBHPHGLQLES---VSFVSMKGEKSHSG 533
QY 534 SKFWKALRLALPLRSLSSAGSNES 558
DB 534 SKFWKALRLALPLRSLSSAGSNES 558
QY 536 GFWKQLOVAMPVKK---SPRWGSN 557
DB 536 GFWKQLOVAMPVKK---SPRWGSN 557

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RESULT 3
ID 063621 PRELIMINARY; PRT; 570 AA.
AC 063621;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, last annotation update)
DE Interleukin-1 receptor accessory protein.
GN IL-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
P SEQUENCE FROM N.A.
MEDLINE=96265355; Pubmed=8964912;
Liu C., Chalmers D., Maki R., De Souza E.B.;
"Rat homolog of mouse interleukin-1 receptor accessory protein:
cloning, localization and modulation studies.";
RT J. Neuroimmunol. 66:41-48(1996).
RL EMBL, U48592; AAB03502.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR004075; IL1_receptor1.
DR InterPro: IPR000157; TIR_domain.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PR01537; INTERLKN1RF.
DR SMART: SM00409; Ig_2.
DR SMART: SM00255; TIR; 1.
KM Receptor.
SQ SEQUENCE 570 AA; 65598 MW; 20C3A5478127AABE CRC64;

Query Match 63.1%; Score 2313.5; DB 11; Length 570;
Best Local Similarity 75.7%; Pred. No. 8.2e-188;
Matches 430; Conservative 62; Mismatches 55; Indels 21; Gaps 5;

QY 1 MTLKCVSLYFYGIQSDASERCDWGLDTMROIOVFEDPARIKCPLEFHLKKNYST 60
DB 1 MGLPWCMLSLFCGILQSHASERCDWGLDTMROIOVFEDPARIKCPLEFHLKKNYST 60
QY 61 AHSAGLTILMYTRORDLEEPINFLPENRISKEKDVLMFRPTLLNDNGNTCMLRNTT 120
DB 61 AHSAGLTILMYTRORDLEEPINFLPENRISKEKDVLMFRPTLLNDNGNTCMLRNTT 120
QY 121 YCSKVAFLPEVVOKSCFNSPMKLPHKLYIEGIORITCPNVGYPSSVKPTITWYG 180
DB 121 YCSKVAFLPEVVOKSCFNSPMKLPHKLYIEGIORITCPNVGYPSSVKPTITWYG 180
QY 181 CYKIQNFNNVIRPGNMLSPILALISNNNGYTCVYTPENGRTFHLTRTLTVKVGSPKNA 240
DB 181 CYKIQNFNNVIRPGNMLSPILALISNNNGYTCVYTPENGRTFHLTRTLTVKVGSPKNA 240
QY 241 VPPVHISPDHVVYEKEPEBELLIPCTVYFSLMDSRNEVWMTIDKKDDITIDVTINE 300
DB 241 VPPVHISPDHVVYEKEPEBELLIPCTVYFSLMDSRNEVWMTIDKKDDITIDVTINE 300
QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAGKGVAKAAVKKQVAPRYTEL 360
DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAGKGVAKAAVKKQVAPRYTEL 360
QY 361 ACQFGATVLLVYLIVYHYVLEMLFPAHAGTDETTIDGKXYDIYVSARNAEEBF 420
DB 361 ACQFGATVLLVYLIVYHYVLEMLFPAHAGTDETTIDGKXYDIYVSARNAEEBF 420
QY 421 VLLTAGVENERGYKCLFDRSLPGQNTVEAVPDFIORSRMIVLSDVYTERKSI 480
DB 421 VLLTAGVENERGYKCLFDRSLPGQNTVEAVPDFIORSRMIVLSDVYTERKSI 480
QY 481 LBEKGLGVMCONSIAIK-----LIVERYRPLEHPHGIQLQKE-----SVSFVSKGKSK 530
DB 481 LBEKGLGVMCONSIAIK-----LIVERYRPLEHPHGIQLQKE-----SVSFVSKGKSK 530

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DB 481 LBEKGLGVMCONSIAIK-----LIVERYRPLEHPHGIQLQKE-----LKVKEIKRAKSVLTIKMGKSK 532
QY 531 HSGSKFPMKALRALPLRSLASAGWNES 558
DB 533 YPGRFWKOLQVAMPYK-----SPRWSS 557

RESULT 4
ID 09NPH3 PRELIMINARY; PRT; 356 AA.
AC 09NPH3;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, last annotation update)
DE Soluble interleukin 1 receptor accessory protein (Soluble interleukin-1 receptor accessory protein).
GN IL1RAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
P SEQUENCE FROM N.A.
MEDLINE=20261666; Pubmed=10799899;
Jensen L.E., Muzio M., Mantovani A., Whitehead A.S.;
"IL-1 signaling cascade in liver cells and the involvement of a
soluble form of the IL-1 receptor accessory protein.";
RT J. Immunol. 164:5277-5286(2000).
RL EMBL, AF167340; AAF71688.1; -.
DR EMBL, AF167340; AAF71688.1; -.
DR EMBL, AF167335; AAF71688.1; JOINED.
DR EMBL, AF167336; AAF71688.1; JOINED.
DR EMBL, AF167337; AAF71688.1; JOINED.
DR EMBL, AF167338; AAF71688.1; JOINED.
DR EMBL, AF167339; AAF71688.1; JOINED.
DR EMBL, AF167343; AAF71687.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00409; Ig; 2.
KM Receptor.
SQ SEQUENCE 356 AA; 41019 MW; 39B72452C458A1C3 CRC64;

Query Match 51.6%; Score 1892; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 2.7e-152;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLKCVSLYFYGIQSDASERCDWGLDTMROIOVFEDPARIKCPLEFHLKKNYST 60
DB 1 MTLKCVSLYFYGIQSDASERCDWGLDTMROIOVFEDPARIKCPLEFHLKKNYST 60
QY 61 AHSAGLTILMYTRORDLEEPINFLPENRISKEKDVLMFRPTLLNDNGNTCMLRNTT 120
DB 61 AHSAGLTILMYTRORDLEEPINFLPENRISKEKDVLMFRPTLLNDNGNTCMLRNTT 120
QY 121 YCSKVAFLPEVVOKSCFNSPMKLPHKLYIEGIORITCPNVGYPSSVKPTITWYG 180
DB 121 YCSKVAFLPEVVOKSCFNSPMKLPHKLYIEGIORITCPNVGYPSSVKPTITWYG 180
QY 181 CYKIQNFNNVIRPGNMLSPILALISNNNGYTCVYTPENGRTFHLTRTLTVKVGSPKNA 240
DB 181 CYKIQNFNNVIRPGNMLSPILALISNNNGYTCVYTPENGRTFHLTRTLTVKVGSPKNA 240
QY 241 VPPVHISPDHVVYEKEPEBELLIPCTVYFSLMDSRNEVWMTIDKKDDITIDVTINE 300
DB 241 VPPVHISPDHVVYEKEPEBELLIPCTVYFSLMDSRNEVWMTIDKKDDITIDVTINE 300
QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAGKGVAKAAVKKQ 350
DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAGKGVAKAAVKKQ 350

RESULT 5
ID 08VCB9

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ID 08VCB9 PRELIMINARY; PRT; 360 AA.
AC 08VCB9;
DT 01-MAR-2002 (Tremblere1.20, Created)
DT 01-MAR-2002 (Tremblere1.20, Last sequence update)
DT 01-JUN-2002 (Tremblere1.21, Last annotation update)
DE Similar to interleukin 1 receptor accessory protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
DR EMBL; BC021159; AA021159.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 3.
KM Receptor.
SQ SEQUENCE 360 AA; 41567 MW; B525471759FF7719 CRC64;
Query Match 45.3%; Score 1663; DB 11; Length 360;
Best Local Similarity 85.1%; Pred. No. 7, 66-133;
Matches 298; Conservative 30; Mismatches 22; Indels 0; Gaps 0;
QY 1 MTLIMCVSLFYGILOSADSEKCDMDGLDTRQIQVFEDEPARIKCPLEHFLKFNYS 60
DB 1 MGLIMVSLFYGILOSADSEKCDMDGLDTRQIQVFEDEPARIKCPLEHFLKFNYS 60
QY 61 AHSAGLTLIWMYTRORDLEEPINRLPENRISKEDVLMFRPLNDTGNVTCMLRNT 120
DB 61 AHSAGLTLIWMYTRORDLEEPINRLPENRISKEDVLMFRPLNDTGNVTCMLRNT 120
QY 121 YCSKVAFLPELVOKDS-CFNSPMKLPVHKLVEYGIQRTCPNVNGVFPSSVKPFTITWYG 180
DB 121 YCSKVAFLPELVOKDS-CFNSPMKLPVHKLVEYGIQRTCPNVNGVFPSSVKPFTITWYG 180
QY 181 CYKIQNFNNVPIEGMNLSPILALISNNNGNTCVVTPENGRTFLTRTLVYKVGSPRPA 240
DB 181 CYKIQNFNNVPIEGMNLSPILALISNNNGNTCVVTPENGRTFLTRTLVYKVGSPRPA 240
QY 241 VPIIHSNPHVYVEKEGEBELIPCTVYPSFLMDSREVMWTTIDGKKDDITIDVTINE 300
DB 241 LPIPIYSPNDVYVEKEGEBELIPCTVYPSFLMDSREVMWTTIDGKKDDITIDVTINE 300
QY 301 SISHRTEDTRTQILSIKVTSEDLKRSYVCHARSAKGEVAKAKVKK 350
DB 301 SVSSTSEDETRTQILSIKVTSEDLKRSYVCHARSAKGEVAKAKVKK 350

RA Sana T.R., Debets R., Timans J.C., Bazan J.F., Kastelein R.A.;
RT "Computational identification, cloning and characterization of IL-1R9,
RT a novel interleukin-1 receptor (IL-1R)-like gene encoded on human
RT chromosome Xq 22.2-22.3";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Grabowski M., Lorenz B., Hubel R., Strom T.M.;
RT "A gene (IL1RAPL-2) with 61% identity to IL1RAPL maps to Xq22.2";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20459050; PubMed=10882729;
RA Born T.L., Smith D.E., Gaika K.E., Renshaw B.R., Bertles J.S.,
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling";
RL J. Biol. Chem. 275:29946-29954(2000).
DR EMBL; AJ290436; CAB89867.1; -
DR EMBL; AF212016; AA61307.1; -
DR EMBL; AF212208; CAB86868.1; -
DR EMBL; AF284436; CAB21370.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR00157; TIR_domain.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNRI1P.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00255; TIR; 1.
KM Receptor.
SQ SEQUENCE 686 AA; 78669 MW; E400F7ECD166957C CRC64;
Query Match 22.5%; Score 825; DB 4; Length 686;
Best Local Similarity 31.9%; Pred. No. 2, 9e-61;
Matches 228; Conservative 106; Mismatches 244; Indels 136; Gaps 27;
QY 1 MTLIMC-VSLFYGILOSADSEKCDMDGLDTRQIQVFEDEPARIKCPLEHFLKFNYS 59
DB 7 LALVVCVSVSNLKMVSRSVDCIDMSVD-LKTVALAGEPRVCAALYSTIRNYS 65
QY 60 TAHSAGLTLIWMYTRORDLEEPINRLPENRISKEDVLMFRPLNDTGNVTCMLRNT 119
DB 66 TAQSTGLRLMY--KNGGDLEPIIF--SEVRMKEDSITPHSAEADSGFTYCLRNS 121
QY 120 YCSKVAFLPELVOKDS-CFNSPMKLPVHKLVEYGIQRTCPNVNGVFPSSVKP 173
DB 122 TYCMKVSMSLTVAEENSGLCYNSRIR-----YLEKSEVTYKKEISCPMDDFKKSQDEP 175
QY 174 TITWYMGYKIQNFNNVPIEGMNLSPILALISNNNGNTCVVTPENGRTFLTRTLVYK 233
DB 176 DVVWYKECKEPRMRSIILIQGNALLIOEVOBEGDGNITCEKTY--EGTL--VRRITELKV 231
QY 234 VGSPPKNAV-PVHSNPHVYVEKEGEBELIPCTVYPSFLMDSREVMWTTIDGKKDDI 292
DB 232 TALITDPRPDLPMENQPSVIDQGLKPLINIPCKAFGSGSGPMIYW-MNGEK----- 286
QY 293 TIDVTINESISHRTEDTR-----TQILSIKVTSEDLKRSYVCHARSAKGEV 341
DB 287 ----FIELLGHIR-EGEIRILKEHLEKEKEVALILIDPSVEADL-ANYCHVENRNGR- 339
QY 342 AKAKVKKQVAPRYTVELACGFATVLVILIVVHVHVMVLFYRAHFGDTEILD 401
DB 340 -KASVLLRKQDLIKYKIELAGLGFILFLVILVYIKYCNITELMFLYRQHPGADRTND 398
QY 402 GKEYDIYVSAR-----NAEEEFVLLTLRGVLENERGYGLCFDRDSLPGANTVE 452
DB 399 NKEYDAVISTYKVDQDGLDCDNPPEEQPALVLPDVLEKHYGYLPIPRDLIPSGTYME 458

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Qy 453 AVDFPQRSRMIVLSPDYTERKSIQMLERKLGVMCONSIAI---KLIVERYPLEHPH 509
Dy 459 DLFYVQSRRLIIVLPDYLRGWSI--FELESRLHMLVSGEIKVILECTELK--- 513
Qy 510 PG-----ILQKESV---SFSWKGEKSKHSGKFWKALPLALPLR----- 547
Dy 514 -GKVCQEVESIKRSIKLILIKMGSKSKSLKNSKFWKHLVYEMPIKKEMLPRCHVLS 572
Qy 548 -----SLSSSGNNESSCOSDLSLHVQRRLRRLKEPPELQSS----- 586
Dy 573 AEQGLFGELOPIPSIAIMTSTSLVSSQADL-----PEFHSDSMQIRHC 617
Qy 587 -----EPAAGSPAPGKMSKRGKSATRCCTVYCEGHNLRN--KSRAEIH 632
Dy 618 CRGYKHEIPATLTPVPPLSGNH-----TYCNLPITLNGQLPLANNYLKDOEFH 666

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JLT 7

Q9NZNO PRELIMINARY; PRT; 658 AA.

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AC Q9NZNO;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE X-linked interleukin-1 receptor accessory protein-like 2
DE (Fragment).
GN IL1RAPL2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20218565; Pubmed=10757639;
RA Jin H., Visesvarajah R., Gardner R.J., Roberts R.G.;
RT "Two novel members of the interleukin-1 receptor gene family, one
RT deleted in Xp21.3-Xp21.3 mental retardation.";
RL Eur. J. Hum. Genet. 8:87-94(2000).
DR EMBL; AF181285; AAF59412.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003600; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR000157; TIR_domain.
PFam; PF00047; Ig_3.
PFam; PF01562; TIR; 1.
SMART; SM00409; IG_2.
SMART; SM00410; IG_1like; 1.
DR SMART; SM00255; TIR; 1.
KM Receptor.
FT NON_FER
SQ SEQUENCE 658 AA; 75626 MW; 5B7506AF1110B12 CRC64;

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Query Match 22.3%; Score 817.5; DB 4; Length 658;
 Best Local Similarity 32.3%; Pred. No. 1,2e-60;
 Matches 223; Conservative 99; Mismatches 233; Indels 135; Gaps 26;

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Qy 24 CDWGLDYMTOIQVFEDEPARIKCPLEFHLKFNYSRAHSGTLIWMYTRQDDLEBPI 83
Dy 3 CIDMSVD-LKTYMALAGEPVKCALFFSYIRTVYSTAOSTGLRLMWY--KNGDLEBPI 59
Qy 84 NFRLPERISKEKQVLMFRPTLNDTNGNTYCMLENTYCSVNAFPLEVQDS--CENSP 141
Dy 60 IF--SEVMSSEEDSIFMFSAEADDSGYTCTVLNSTYCMKMSLTYVAENBSGLCYNSR 117
Qy 142 MKLPVHLVIEYVG---IORITCPNVQDYPFSSVYKPTITWYMGCYKIQNFNNVPEGMNL 197
Dy 118 IR-----YLEKSEVTKRKEISCPDMDPKSKDDEPPVWYKCKPKKMSIILQKGNAL 171
Qy 198 SFLLALISNNQNTCVVTPYNGRTFHLTRTLTVKVGSSPNAVP-PYHSPPNDHYEK 256
Dy 172 LIGVEGDEGNGNYTCELKY--EGKL--VRRTTELKVTALLTDKPKPLFPMENQPSYIDV 227

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Qy 257 EPGELLIPCTVYFSLMDSRNEVMWTIDGKRPDITIDVTINESISHRTEDETR---- 312
Dy 228 QLGKPLMIPCKAPFGFGESGPMIYW--MKGEK-----FIEBLAGHIR-EGEIRLLKE 277
Qy 313 -----TQLSTIKQTSSEDLKSYVCHASAKAEVAKAKVQKQVAPRTVYLACFG 365
Dy 278 HLGEKEVELLIPDSVVEADL--ANYTCHVENRNGR--KHASVLLRKDOLYKIELAGLG 334
Qy 366 ATVLVAVILIVVHVAVLEWLFYRAHGTDETLIDKEVQIYVSAR-----NAE 416
Dy 335 AIFLLVAVLVYIKVAVIEMLFROHFGADEINDNKSDAYLTKVVDOTLDCDNPE 394
Qy 417 EEEFVLLTLRGVLENERGYKLCIFDRDSLPGNTVEAVDFPQRSRMIVLSPDYTERK 476
Dy 395 EEOGPALEVLDPVLEKHGYKLFIPERDLIPSGTWMEDLTRVVEGSRRLIIVLTPDYILR 454
Qy 477 SISMLERKLGVMCONSIAI---KLIVERYPLEHPHQ-----ILQKESV---SFSW 524
Dy 455 GWSI--FELESRLHMLVSGEIKVILECTELK-----GKVCQEVESIKRSIKLILIKW 508
Qy 525 KGEKSKHSGSKFWKALPLALPLR-----SLSSSGNNESS 558
Dy 509 KGSKSKSLKNSKFWKHLVYEMPIKKEMLPRCHVLSABQGLFGELOPIPSIAIMTSTSL 568
Qy 559 CSQSODISLDHVQRRLRRLKEPPELQSS-----EPAAGSPAPGKMSKRG 604
Dy 569 VSSQADL-----PEFHSDSMQIRHCRCRGYHLEIPATLTPVPPLSGNH-- 611
Qy 605 KKSATRCRCCTVYCEGHNLRN--KSRAEIH 632
Dy 612 ---TYCNLPITLNGQLPLANNYLKDOEFH 638

```

RESULT 8

Q9ERS6 PRELIMINARY; PRT; 686 AA.

```

AC Q9ERS6;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE TIGIRR-1.
GN IL1RAPL2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20459050; Pubmed=10882729;
RA Born T.L., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.,
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling.";
RL J. Biol. Chem. 275:29946-29954(2000).
DR EMBL; AF284437; AAG21371.1; -.
DR MGD; MGI:1913106; Il1rapl2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003600; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR000157; TIR_domain.
PFam; PF00047; Ig_3.
PFam; PF01562; TIR; 1.
SMART; SM00409; IG_2.
SMART; SM00410; IG_1like; 2.
DR SMART; SM00255; TIR; 1.
SQ SEQUENCE 686 AA; 78797 MW; 36160D1CDB9B8264 CRC64;

```

Query Match 22.0%; Score 806.5; DB 11; Length 686;
 Best Local Similarity 32.5%; Pred. No. 1.1e-59;
 Matches 215; Conservative 107; Mismatches 255; Indels 85; Gaps 24;

Qy 1 MTLIMC-VVSLYFYGLIQSDASERCDWGLDYMTOIQVFEDEPARIKCPLEFHLKFNYS 59

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Db      7 LALVCSAATVTLKAVSKNSVDGCTDMSVD-LKTMALAGEVVRKCALFYIITNTS 65
Qy      60 THASGLTILWTRDRLDLEEPINRLPENRISKEDVLMFRPTLLDNTGNTCMRLNT 119
Db      66 MAOSTGLRLMWY--RMKGLLEBIIIF--SEVRMSKEEDALMFHASAEODSGFYTCVLANS 121
Qy      120 TCSVAAPLEVVOKDS--CFNSPMLPVHKYIEYG----IQRICPNVDGFPSVYK 173
Db      122 TCMKVSMLTYAENESGCTNSRIR-----YLEKSVTKREKISCDDDDPKSDQEP 175
Qy      174 TITWMCYKIQNFNNVIEGNNLSFLIALISNNGNVTCVVYTPENGRTFHLTRTLTVKV 233
Db      176 DVVWYKECKPKMWRSLIIQGNALLIQEVEHGGNYTCELK--BGKL--VARTELKV 231
Qy      234 VCSKPAVPEVIVHNSNDVYKEKEGEBLLIPCTVYPSFLMSDNEVWMTIDGKPPDI 292
Db      232 TALLTDKPKPLPPEMNOPIVDVQKPLNIPCKAFPGSGSGPMIYW-MKGEK---- 286
Qy      293 TIDVTINESISHRTEDTR-----TQIISIKKVTSDIKRSYVCHARSAGV 341
Db      287 ----FIEELAGIIR-EGEIRLKLKELGKVEVETLIPDSVEADL-ANTYCHVENNGR- 339
Qy      342 AKAAVKOKVAPARYVELACGATVLLVILIVVHVWLMVLFYRAHFGTDETLID 401
Db      340 -KHAIVLARKKOLIKIELAGLGALFLLIILVYKCYNIHMLFTQRFGSDTTDD 398
Qy      402 GKEDIVYVSAR-----NAEEBFPVLLTRGVLENEFGYKLCIPDRSLPGNTVE 452
Db      399 NKEVDAYISYTKVQDDTLDCDNTVEEQFALIELPDLVLEHGYKLPIDRDLIPSGTYIE 458
Qy      453 AVFDIORSRMIVVLSPDVYTEKISMLPEFKLGWCONSIAT--KLIVERYRLEHHPH 509
Db      459 DITRCVEOSRRLIVLTPDYILRRGWSI--FELSRILNMLVSGELIKVILIECTELK--- 513
Qy      510 PG-----ILQIKESV--SFVSMGKESKSHSGKFKMALARLPLRSLASAGNMSGS 560
Db      514 -GKVVCGEVESLKHNIKLISLIMKQPKSKLNSKPMKLVYEMPIKKEMLSHCVALDS 572
Qy      561 SOSDISLDHVORRSRLKEPPELOSSERAAGSPAPAGMSKIRGKSATCRCCVYCEB 620
Db      573 AEOGIF-----GELQIPISIAMTSTSATVPSQADLPETIHSDSMQMRIC---CRGY 621
Qy      621 NH 622
Db      622 QH 623

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RESULT 9
Q9NZNI PRELIMINARY: PRT: 696 AA.

Q9NZNI;
01-OCT-2000 (Tremblrel. 15, Created)
01-OCT-2000 (Tremblrel. 15, Last sequence update)
01-JUN-2002 (Tremblrel. 21, Last annotation update)
X-linked interleukin-1 receptor accessory protein-like 1.
IL1RAPL1.
Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=20218565; PubMed=10757639;
RA Jia H., Vismasvaratah R., Gardner R.J., Roberts R.G.;
RT "Two novel members of the interleukin-1 receptor gene family, one
deleted in Xp21.3-Xp21.3 mental retardation.";
RL Eur. J. Hum. Genet. 8:87-94(2000).
DR EMBL, AF181284; AAF59411.1;
DR InterPro: IPR003598; 19_C2.
DR InterPro: IPR004006; 19_MHC.
DR InterPro: IPR004075; IL1_receptor1.
DR InterPro: IPR000770; SAND_domain.
DR

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DR      InterPro: IPR000157; TIR_domain.
DR      Pfam: PF00047; ig_2.
DR      Pfam: PF01582; TIR; 1.
DR      PRINTS: PR01537; INTRLNRI1P.
DR      SMART: SM00408; IGC2; 1.
DR      SMART: SM00258; SAND; 1.
DR      SMART: SM00255; TIR; 1.
DR      Immunoglobulin domain; Receptor.
DR      KX
SEQUENCE 696 AA; 79979 MW; F2EBCC37153799AA0 CRC64;
SQ
Query Match      21.0%; Score 769.5; DB 4; Length 696;
Best Local Similarity 29.0%; Pred. No. 1.5e-56;
Matches 206; Conservative 127; Mismatches 287; Indels 91; Gaps 21;
Qy      1 MTLNCSVSLVYGYGLQSDASERCDWGLDTRQIQVEDEPARIKCPLFEHFLKFNST 60
Db      8 LILVATFTQSLKXYTKGASADGCTDMSID-IKKYQVAVGEVRIKCALFYGYIRNTSL 66
Qy      61 ASAGLTILWTRDRLDLEEPINRLPENRISKEDVLMFRPTLLDNTGNTCMRLNT 120
Db      67 AOSAGLSLWYKSGSGPGDFEPIAF--DGSRMSKEEDSIWFRPTLLQDGLVACVIRNST 124
Qy      121 YCSKVAAPLEVVOKDS--CFNSPMLPVHKYIEYG----IQRICPNVDGFPSVYK 174
Db      125 YCMKVISLTVGENDTGCTNSKMK-----YFEKAEISKSEISCRDIEDFLPTRBEP 178
Qy      175 ITWMCYKIQNFNNVIEGNNLSFLIALISNNGNVTCVVYTPENGRTFHLTRTLTVKV 234
Db      179 ILWYECRTKTRPSIVKRPDILLREVREDIGNYTCELK--GQFVARTTELTVT-- 234
Qy      235 GSPKPAVPEVIVHNSNDV--VYKEKEGEBLLIPCTVYPSFLMSDNEVWMTIDGKPPDI 292
Db      235 -APLTDKPKPLYPWESKLTIOETQDGSANLTCRAFGYSGDVAPLLYMMKGEKFIEDL 293
Qy      293 ----TIDVTINESISHRTEDTRTQIISIKKVTSDIKRSYVCHARSAGVAKAK 346
Db      294 DENRVESDITR--LKEHLGEOEVSISLI--VDSVEBDL-GNVSQVYENNGR--RHAS 346
Qy      347 VKOKVAPARYVELACGATVLLVILIVVHVWLMVLFYRAHFGTDETLIDGKED 406
Db      347 VLMHRELMVVELAGLGALILLVCLVYIKCKEIMLFYRNHFGAELDGNKOYD 406
Qy      407 IYVSAR-----NAEEBFPVLLTRGVLENEFGYKLCIPDRSLPGNTVAVPDF 457
Db      407 AYLSTYKVPQWNOGETEERFALIELPDLMEKHGYKLPIDRDLIPGTIYIDVAVRC 466
Qy      458 IQRSRMTVLSPDVYTEKISMLPEFKLGWCONSIAT--KLIVERYRLEHHPGLQ 514
Db      467 VDQSRLLIIVMTPNVTVRRGWSI--FELSTRRLNMLVTGEIKVILIECSELR---GIMN 520
Qy      515 LKE-----SVSFVSMGKESKSHSGKFKMALARLPLR----- 547
Db      521 YQEVVALKHTIKLIVIMHPKCKNLSKPMKLVYEMPIKKEMLSHCVALDS 580
Qy      548 --SISASGMSGSGSDISLDVQR-----RSFLKEPPELOSSERAAGSPAPAGX 598
Db      581 FGELOTVSAISMAAATSTALATAPDLSTYHNTYHSQMRQHYRSEYEVV--PPTGTL 638
Qy      599 MSKIRGKSATCRCCVYCEENHLMKRSRAHINOPWETHLCKPVQES 649
Db      639 PLTSGNQHYYCNIPMLINDGROPQYSSRQNDPEAHNTSAILPLPRET 689

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RESULT 10
Q9U53 PRELIMINARY: PRT: 696 AA.

Q9U53;
01-MAY-2000 (Tremblrel. 13, Created)
01-MAY-2000 (Tremblrel. 13, Last sequence update)
01-JUN-2002 (Tremblrel. 21, Last annotation update)
Oligohemerin-4 (TIGR-2).
GN OPN4.
Homo sapiens (Human).


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Db 6 LILTLICI-----LIVSASKSCIH-----RSQIHVVEGEFPYKPCGISAPVIRN--- 50
Qy 56 FNVSTASHAGLTLVWTRORDLEEPINFLPENRISKEDVLMFRPTLNDNTNYCM 115
Db 51 ---ETA-----TMRWFKSGASHRELNRRSP--RVTFHDHTLEFWPEWEDGETYISQ 100
Qy 116 LRNTTYSKVAFLPEVVO--KDSCFNSPMKLFVHKLTYEYGIO-----RTTC--PNVGY 166
Db 101 VGN-----DRRWTLNVTGRNGHSCSD-----KLVTSDVEVKKSLHTCKNPNYSEL 149
Qy 167 PPSVSKPTITW--YMGCYKIQNFNNVPEGMNLSFLIALISNNGNTCVVYTPENGRTFL 225
Db 150 IOD-----TWLYKNCKEISKTPRIKID-----AERGDEGYSCVFSVHNGCTRNI 195
Qy 226 TRITLVKVGSPKNAVPPVISHPNHVYKEKPEGELLIPCTVYFSFLMDSNENWMTID 285
Db 196 TKTVNITVI--EGRSKVTPLALGPKCEKV--GVELGQVEILNC-----SASLMDKDLFYMSI- 248
Qy 286 GKXPDITIDVTINESISHSRTEDT-----RTQILSIKVTSEDLKSYVCHARSA 337
Db 249 -RKED-----SSDPNVEDRKETTWTWSEGLHASKILRFQKITEENTIANVLNCTVANE 301
Qy 338 KGEVAKAKVOK--VPAPRYVELACGEGATVIL-----VILIVVHYVYVLEM 385
Db 302 EADPTKSFVLVRKEIPDIRGHVFT-----GGVTVLVASVAACIVILCVIYKV---DL 352
Qy 386 VLFPRAHGTDETIIDKEVDIYVSAR---NABEEFVLLTLRGVLENEFGYKLCIF 440
Db 353 VLFPRRIARDEBTLDGKYAFVSYLKECPENKEEYFAETTLPRVLEKQFGYKLCIF 412
Qy 441 DRDLSRGNTVEAVPDFIORSRMTIVLSPOVTEKISIMLEFKL--GVMCONSITKILIV 499
Db 413 ERDVAPGAVAVEHISLLEKSRRLITVLSOSTLTNGARRELSGHEALVEKKI--KILL 470
Qy 500 VEYRPLEHPH--PGIILQKESVFSVMKGEKSKHSGKFWKALRLALPLRSLSASSGANE 557
Db 471 IEFPPASITFLPSPILKILKSYRVLWKRAD--SPSNKSRFWKLVYLMRAKAVKP---WRE 526
Qy 558 SCSSOSDIS 566
Db 527 ESEARSVLS 535

RESULT 14
1208
AC Q05208 PRELIMINARY; PRT; 567 AA.
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE ST2L protein precursor.
GN ILRL1 OR ST2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93170492; PubMed=7916701;
RA Yanagisawa K., Takagi T., Tsukamoto T., Tetsuka T., Tomimaga S.;
RT "Presence of a novel primary response gene ST2L, encoding a product
RT highly similar to the interleukin 1 receptor type 1."
RL FEMS Lett. 318:83-87(1993).
DR EMBL; D13695; BAA02854.1; -.
DR MGD; MGI:98427; 111r11.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR004075; IL1_receptort1.
DR InterPro; IPR002052; N6_Mtease.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF01582; TIR; 1.

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DR PRINTS; PR01537; INTRLNRI.F.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 567 ST2L PROTEIN.
SQ SEQUENCE 567 AA; 64801 MW; 9228CE227D95B0BC CRC64;

Query Match 13.04; Score 478; DB 11; Length 567;
Best Local Similarity 25.94; Pred. No. 6,7e-32;
Matches 163; Conservative 105; Mismatches 227; Indels 134; Gaps 28;

Qy 4 LM--CVSLVYFGYGIQSDASERCDMDGIDTMRQIQVEDEBARIKCPLEHFLKFNYSYA 61
Db 9 LMAALITLPMY--LITVEGSK--SSKGL-----ENELIYRCP-----QGRST- 49
Qy 62 HSAGLTIWTRORDLEEPINFLPENRISKEDVLMFRPTLNDNTNYCMLRNTTY 121
Db 50 ---YPEWYVS-----DTNESIPTQ--KRNRIFVGRDRKFLPARVEBGIVACYRSPNL 100
Qy 122 CSKVAFLPEVVOQDSRNSPMKLFVHKLTYEYGIO-----ITCPNVGIFPSSVYKPT 174
Db 101 NKTGYLWVTHHKKEPPSCNIPD-----YLMYSTVRGSDKNKFKITCPTIDLY--NWTP 150
Qy 175 ITWYMGCYKIQN-----FNNVPEGMNLSFLIALISNNGNTCVVYTPENGRTF 223
Db 151 VQWFKNCALQEPFRRAHRSYLFIDNVTHD-----DRQDYTCQTHANGNTNY 198
Qy 224 HLTRTLVKKVGSBKNAVPPVISHPNHVYKEKPEGELLIPCTVYFS--FLMDSNNE 279
Db 199 IVTATRSFTVEKSPSMFPVITNPYNHTM--EVEIGKPAISACACPKSGSHPLAD----- 253
Qy 280 VMTIDGKXPDITIDVTINESISHSRTEDT-----TRQILSIKVTSEDLK 327
Db 254 VLM-----QINKTVVGNFGEARIOEEEGNESSNDMDCLTSVLRITGTEKPLS 303
Qy 328 RSYVCHARSAKGEVAKAKVOKVAPARYTV--ELACGATVILVILIVVHYVYVLEMV 386
Db 304 LEYDCLALNLMGMTRIHRLERKOPIDHRSIYIVAGCSLLMTNLTNVLVYLVAKFWMEVA 363
Qy 387 LFPYRHFCTDETIIDKEVDIYVSAR---NABEEFVLLTLRGVLENEFGYKLC 438
Db 364 LFMWDIYTPYKTRNDGKLYDAYIIPRVFRGSACTHSVEYFVHTLTPDVLENNCGYKLC 423
Qy 439 IFDRDSLPGNTVEAVPDFIORSRMTIVLSP-----DYTEKISIMLEFKLGVMCONS 492
Db 424 IYGRDLLPGQDAATVVESSIONSRQVFLVAPHNMHSKEFAVEQDIAL---HSLALIONN 479
Qy 493 IATLIVYERPL--EHRHPGILQKESVSF-----VSMKGE--KSGHS--GSKFWKALR 541
Db 480 --SKVILIEMLPEBASRLQYGDLSLQHLVKIQGTIKMREDHVADKQSLSSKFWKHVR 537
Qy 542 LALPL--RLSLASGNNSSCSQSDISLDH 569
Db 538 YQMEVPERASTKTSVAAPLSGKACLCLKH 566

RESULT 15
09TV71
ID 09TV71 PRELIMINARY; PRT; 573 AA.
AC 09TV71
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Interleukin-1 receptor type 1 precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Kirisawa R., Hashimoto N., Sakamoto C., Enya S., Hagiwara K., Iwai H.;

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RT "Molecular characterization of the equine type I interleukin-1
receptor cDNA."

RL Submitted (NOV-1998) to the EMBL/Genbank/DBD databases.

DR EMBL; AB020338; BAA83730.1; -.

DR HSP; P14778; IIR.

DR InterPro; IPR003600; Ig_1ike.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR004076; IL1R_receptor.

DR InterPro; IPR004075; IL1_receptor1.

DR InterPro; IPR004074; IL1_receptor1/1.

DR InterPro; IPR000157; TIR_domain.

DR Pfam; PF00047; TIR; 1.

DR PRINTS; PR01538; INTERLEUKIN1.

DR PRINTS; PR01536; INTERLEUKIN12F.

DR PRINTS; PR01537; INTERLEUKIN1P.

DR SMART; SM00410; IG_1ike; 2.

DR SMART; SM00255; TIR; 1.

KM Receptor; Signal.

FT SIGNAL 1 20

FT CHAIN 21 573

SEQUENCE 573 AA; 65766 MW; 25703365A89B230B CRC64;

POTENTIAL.

MATURE INTERLEUKIN-1 RECEPTOR TYPE I.

Query Match 13.0%; Score 477.5; DB 6; Length 573;

Best Local Similarity 25.8%; Pred. No. 7.5e-32;

Matches 153; Conservative 120; Mismatches 224; Indels 97; Gaps 27;

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QY 4 LMCVSVLYYYGILQSDASRCDDWGLDMRQIQVFEDEPARIKCPLEHFLKNYSTAHS 63
DB 7 LVCFLIAL----LISLEADKCEERGEPIVIVSAYRIDVR--SCPL-----NPNB 50
QY 64 AGLTLIYWTQRDRLDEPINFRLPENRISKEQVLMFRPTLLNDGNTYCMLEPTTYS 123
DB 51 SNGTIIWY----KNDSETPVSMK--KDSRIHQYDKLWVPAKIEDSGHYCAVRNSTYCL 105
QY 124 KVAFLPELVQ--KDSCEFS----PMKLPMHKLIEYGIORITCPNDGYFPSSVK--PTIT 176
DB 106 KYKITARFQHEPDLQYNQALFTQCLPIG----EDGL--LVCPILEVFRDENNELPKIQ 159
QY 177 WTMGCK--IQPNNVYIPGAMLSFLIALI--SNNGNVTCVVTYPENGRTFHLFRTLTVK 232
DB 160 WYKDCOPLIDNINFI--GKTDKLIIVANVTAHKGHYCHISYTHLGQYPTITVIGLI 216
QY 233 VVGSPKNAVPIVHSPNDHVVVEKEGEELLPCTVYFSEFLMDSRNEVWTTIDGKKPDI 292
DB 217 TIDEIRPTKPLIVSPVNE--TMEVDLGSQVQLCNVTGMF---TDFVYWRNNGSLIDD- 269
QY 293 TIDVTINESI---SHSRTEDETRTQILSIKYVSEDLKRSYVCHARSAKGEVAKAKVK 348
DB 270 -SDPVLVEEYKKEVENSLKRRHTLITVNLISAVESRFYIYPTCLAKNSYGRSAAYVQLR 328
QY 349 QKVPAARYVEELACGEGATVLLVIL--IVYHVMLEMLFYL--AHFGTDETLIDGK 403
DB 339 QEVPPDFQKHV-----IGIFVLLVLAITCSVFYIKLFKVDLVLMYRDSVDFRSPKASDGK 383
QY 404 KYDIYVSVAR-----NAEEEFVLLTLGVLENERGYKLCIPDRDSLPGNTVEAVPDF 457
DB 384 TYDAIYLYKIIIGEGSTNSDIFVFVLPVLEVKQGGYKLFYGRDVGVEDIVEVTNEN 443
QY 458 IORSRRMIVVLSPD-----YTEKSISMLEFKLGVMCONSIAWKLIIVEYRPLEHPH 509
DB 444 IKKSRRLLIILVRETSGLSWLSSSSSEGIAM-----YNALVQDGI--KIILLELEKIQDYE 497
QY 510 PGILQAKESVSFVS-----WKGEKSK--HSGKFTWALRLALPLRSLSSAS 553
DB 498 ---KMPESIKPIKRGHGLRWSGDSRKGPQSAKARFWRNVYRMPVQROLPS 547

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Search completed: April 23, 2003, 08:54:00

Job time : 100 secs